27, Appl 4, Appli 4, Appli 133, App 132, App 1, Appli

Sequence Sequence Sequence 8

US-09-526-098-9 US-09-049-672A-25 US-09-079-029-8 US-08-652-816A-27 US-08-665-202-4 US-09-315-574-4 US-09-240-274-133 US-09-240-274-132 US-08-199-911-1 -08-477-553A-43 -09-240-274-134 -08-264-093-5 US-09-273-839A-9

Sequence

Sequence 4, Sequence 133 Sequence 132 Sequence 1, Sequence 1, Sequence 62,

Sequence

Sequence

ALIGNMENTS

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APPLICANT: RAFF, Mitchell E.
APPLICANT: KLOETZER, William S.
APPLICANT: MICHAURA, TRACHIKO,
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: ANTIBOLIDE CONTROL NUMBER OF SEQUENCES: 35
CORRESPONDERS ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: P.O. Box 1404
CITY: Alexandria
STRATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FEB-1997
CLASSIFICATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
TELECOMMUNICATION HYPORMATION:
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TELECOMMUNICATION PROREMATION:
TELECOMMUNICATION PROREMATICS:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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SEQUENCE CHARACTERISTICS:
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STRANDEDNESS:
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, LOCATION:
US-08-803-085-1
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December 29, 2003, 16:08:50 ; Search time 42.9294 Seconds (without alignments) 4009.823 Million cell updates/sec
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1: /cgn2_6/ptodate/2/ina/5A_COMB.seq:*

1: /cgn2_6/ptodate/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodate/2/ina/6B_COMB.seq:*

4: /cgn2_6/ptodate/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodate/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodate/2/ina/PcTUS_COMB.seq:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-338-933-267
US-10-039-785-59
US-10-039-785-64
US-10-039-785-64
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US-10-039-785-64
US-10-039-785-64
US-10-039-785-60
US-10-039-785-60
US-10-039-785-61
US-10-039-785-55
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Maximum Match 100%
Listing first 45 summaries
                                                                          nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Match Length DB
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2895.2
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DB 3; Length 390;

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TOPOLOGY: line IMMEDIATE SOURCE:
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: You, Henry
APPLICANT: You, Horry
APPLICANT: Ourley, Neil C.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                            ö
                                                            0; Indels
                              Pred. No. 4.3e-106; Mismatches 0;
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SUFTWARE: FastESD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
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20. PF-0497 US
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REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-O
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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                                                               Matches 390; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                 Best Local Similarity
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US-09-049-672A-23
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Sequence 11, Application US/08378939
Sequence 11, Application US/08378939
Sequence 11, Application US/08378939
SEXERAL INFORMATION:
PAPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESSEDE: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THIRTEENTH ST. N.W.
CITYE: MSAINGTON
STATE: D. C.
COUNTRY: U.S.
ZIP: 2000H
MBDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MBDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-COMPATIBLE
SOFTWARE: PREADABLE FORM:
COMPUTER: D. C.
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-COMPATIBLE
SOFTWARE: PARTICLE
COMPUTER: PARTICLE
COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 321.2; DB 3
Pred. No. 1.2e-85;
0; Mismatches 43
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.4%;
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 891 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 89.07
Matches 347; Conservative
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; CLONE: 2872705
US-09-049-672A-23
                                                                                                                                                                                                                              linear
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| NAME/KEY: misc_feature
| LOCATION: (1)...(548)
| CTHER INFORMATION: n = A,T,C or G
US-09-404-879A-267
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 75.7%;
Best Local Similarity 87.7%;
Matches 343; Conservative
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LOCATION: (1)...(548)
                                                                                                                            TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
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ORGANISM: Homo sapien
   NUMBER OF SEQ I
SOFTWARE: Fast
SEQ ID NO 267
LENGTH: 548
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LENGTH: 548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC 180
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APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
CURRENT APPLICATION WHORER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
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Pred. No. 3.5e-85;
0; Mismatches 44
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ATTORNEY/AGENT INFORMATION:

NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEPHONE: (202) 783-6031
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 902 base pairs
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Patent No. 6468546
GENERAL INFORMATION:
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88.7%;
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Matches 346; Conservative
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89..739
                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
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LOCATION:
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FEATURE:
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Sequence 267, Application US/09338933

Patent No. 6488931

GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer Lynn

APPLICANT: King, Gordon E.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF

TITLE OF INVENTION: OVARIAN CANCER

FILE REFERENCE: 210121.46201

CURRENT APPLICATION NUMBER: US/09/338, 933

CURRENT FILING DATE: 1999-06-23

NUMBER OF SEQ ID NOS: 312

SOFTWARE: FREUSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 295.2; DB 4;
Pred. No. 4.9e-78;
0; Mismatches 46;
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US-09-338-933-267
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                          GATCGCTTCTCTGGCTCCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 300
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WESULY 7

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Sequence 59, Application US/10039785

FRETEN NO. 6538981

GENERAL INFORMATION:

APPLICANT: Salcedo et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Acceptors

FILE REFERENCE: PF550

CURRENT FILING DATE: 2002-06-07

FRIOR APPLICATION NUMBER: 60/369,860

FRIOR APPLICATION NUMBER: 60/369,860

FRIOR APPLICATION NUMBER: 60/31,310

FRIOR PILING DATE: 2001-12-20

FRIOR PILING DATE: 2001-11-07

FRIOR FILING DATE: 2001-11-07

FRIOR PILING DATE: 2001-11-07

FRIOR PILING DATE: 2001-10-09

FRIOR PILING DATE: 2001-10-09

FRIOR APPLICATION NUMBER: 60/323,807

FRIOR APPLICATION NUMBER: 60/323,807

FRIOR APPLICATION NUMBER: 60/323,407

FRIOR PILING DATE: 2001-09-21

FRIOR PILING DATE: 2001-09-21

FRIOR PILING DATE: 2001-09-25

FRIOR PILING DATE: 2001-09-25

FRIOR PILING DATE: 2001-06-06

FRIOR PILING DATE: 2001-06-06

FRIOR PILING DATE: 2001-06-25

NUMBER OF SEQ ID NOS: 66

SEQ ID NO 59

LENGTH 735
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                                                                                                                                                                                                                                                                                      360 CGGAAG-AGGGACCCGGTTGACCGTCCTAGG 389
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US-10-039-785-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial sequence
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Best Local Similarity
Matches 310; Conservat
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                                        47 ATGGCCTGGGGCTCTCCTCCTCCTCCTCCTCCTCAGGGCACAGGGTCCTGGGCCCAG
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APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
APPLICANT: Frudakis, Tony N.
APPLICANT: Frudakis, Tony N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS;
TITLE OF INVENTION: OF OVARIAN CANCER;
FILE REFERENCE: 210121.4463
CURRENT APPLICATION NUMBER: US/09/215,681A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOFTWARE: FBSESEQ for Windows Version 3.0
SEQ ID NO 267
LENGTH: 548
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87.7%; Pred. No. 4.9e-78;
tive 0; Mismatches 46
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| LOCATION: (1)...(548)

| CTHER INFORMATION: n = A,T,C or G

US-09-215-681-267
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Best Local Similarity 87.7
Matches 343; Conservative
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ORGANISM: Homo sapien
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -09-215-681-267
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                                                                                                                                                                                                                                                                                          GENERAL INCOMMINION:

JAPPLICANT: Salcedo et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Receptors

FILE REFERENCE: PF550

CURRENT APPLICATION NUMBER: US/10/039,785

CURRENT PILING DATE: 2002-05-07

FRIOR FILING DATE: 2002-04-05

PRIOR FILING DATE: 2001-12-20

PRIOR FILING DATE: 2001-12-20

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-09-21

PRIOR FILING DATE: 2001-09-21

PRIOR FILING DATE: 2001-06-04

PRIOR FILING DATE: 2001-06-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 735;
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220 AAGCGGGCCTCAGGGGTCTCTGATCGCTTCTCTGGCTCCAAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41;
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88.3%; Pred. No. 4.2e-75;
iive 0; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: DNA encoding T1015E01 scFv
US-10-039-785-64
                                                                                                                                                                          S-10-039-785-64
Sequence 64, Application US/10039785
Patent No. 6538938
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.33
Matches 310; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 GGACAGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTAT 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aarcegecercagegerrichaaregerrererecerecaagreregeaacadegeeree 624
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                                                                         625 CTGACCATCTCTGGGCTCCAGGCTGACGAGGCTGATTATTACTGCAGCTCATATACA 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-039-785-63
Sequence 63, Application US/10039785
Patent No. 6538938
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REPERBNCE: PFSSO
CURRENT FILING DATE: 2002-04-05
FRIOR APPLICATION NUMBER: 60/349,860
PRIOR FILING DATE: 2002-04-05
PRIOR FILING DATE: 2001-11-20
PRIOR PRIOR APPLICATION NUMBER: 60/341,237
PRIOR PRIOR APPLICATION NUMBER: 60/341,310
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-09
PRIOR 
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                                                                                                                                                  340 ACCAGTAGCACTTTGTTATTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT
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US-10-039-785-63
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ORGANISM: Artificial sequence
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                                                                                                                                                                                                                                                                                                                                              US-10-039-785-63
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                                                                                                       GENERAL INCOMATION:

APPLICANT: Salcede et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Receptors

FILE REFERENCE: PP550

CURRENT APPLICATION NUMBER: US/10/039,785

CURRENT APPLICATION NUMBER: 0/349,860

PRIOR PILING DATE: 2002-05-07

PRIOR PILING DATE: 2002-04-05

PRIOR PILING DATE: 2001-12-20

PRIOR PLING DATE: 2001-11-14

PRIOR PLING DATE: 2001-11-14

PRIOR PLING DATE: 2001-11-09

PRIOR PLING DATE: 2001-11-09

PRIOR PLING DATE: 2001-11-09

PRIOR PLING DATE: 2001-10-09

PRIOR PLING DATE: 2001-09-01

PRIOR PLING DATE: 2001-06-04

PRIOR FILING DATE: 2001-06-05

PRIOR FI
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US-10-039-785-54
Sequence 54, Application US/10039785 Patent No. 6538938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial sequence
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Sequence 13, Application US/08958201 Patent No. 5977319 GENERAL INFORMATION: APPLICANT: Pope, Anthony R

RESULT 11 US-08-958-201-13

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118 TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 cacccadecaaadcccccaaacrcardarrrrrdaggrcagraarcdgcccrcadggrr 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 cadricidentral de la contraction de la cadricia del cadricia del cadricia de la cadricia del cadricia de la cadricia del cadricia de la cadricia del cadricia
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Pritchard, Kevin
Williams, Andrew J
Johnson, Kevin S,
TENTION: Specific binding members for estradiol;
VENTION: materials and methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/958,201
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .4; DB 2;
3e-72;
ches 36;
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Pred. No. 3e-7:
0; Mismatches
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APPLICATION NUMBER: US 60/028,897
FILING DATE: 21-007-1996
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGHH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Patent No. 2977319
GENERAL INFORMATION:
APPLICANT: Pope, Anthony R
                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 6300 Sears Tower, 233
STATE: Chicago
STATE: 1111nois
CONTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO
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llarity 89.2%;
Conservative (
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                                                    APPLICANT: Williams, And APPLICANT: Johnson, Kev TITLE OF INVENTION: Sperific OF INVENTION: MACHONER OF SEQUENCES: 23 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 297; Conserv
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US-08-958-201-13
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SEQ ID NO 57
LENGTH: 735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATAAGTATGTCTCCTGGTACCAACAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 TCTGATCGCTTCTTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 297
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Patent No. 6538938
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
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TITLE OF INVENTION: Specific binding members for estradiol, TITLE OF INVENTION: Specific binding members for estradiol, TITLE OF INVENTION: materials and methods NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS: ADDRESSEE: Marshall O'Toole Carretter: 6300 Section Corrections Correcti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 333;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/958,201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.2%; Score 273.8; DB 2
88.9%; Pred. No. 8.8e-72;
live 0; Mismatches 37
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,897
FILING DATE: 21-0CT-1996
FILING DATE: 21-0CT-1996
FILING CHARACTERISTICS:
LENGTH: 333 base pairs
TYPE: nucleic acid
CTRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: D12 (light chain)
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Best Local Similarity 88.9
Matches 296; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Illinois
                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Chicago
STATE: Illinoi
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US-08-958-201-11
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280 CTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACA 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Salodo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR PILING DATE: 2002-04-05
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Pred. No. 2.2e-70;
0; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: DNA encoding T1014A12 scFv
US-10-039-785-57
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR PILING DATE: 2001-12-20
PRIOR PILING DATE: 2001-12-20
PRIOR PILING DATE: 2001-11-14
PRIOR PILING DATE: 2001-11-14
PRIOR PILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR APPLICATION NUMBER: 60/332,807
PRIOR PILING DATE: 2001-110-09
PRIOR PILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR PILING DATE: 2001-09-21
PRIOR PILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR SEQ ID NOS: 66
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Patent No. 6538938
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 85.5%;
Matches 300; Conservative
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US-10-039-785-60
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Search completed: December 29, 2003, 21:48:25 Job time: 44.9294 secs
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE SPERSWCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR APPLICATION NUMBER: 60/349,860
PRIOR PILING DATE: 2002-04-05
PRIOR FILING DATE: 2002-12-20
PRIOR PLING DATE: 2001-12-20
PRIOR PLING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR APPLICATION NUMBER: 60/331,044
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Pred. No. 6.6e-70;
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US-10-039-785-60
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PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-09-09
PRIOR PILING DATE: 2001-09-01
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR PILING DATE: 2001-09-02
PRIOR PILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-04
PRIOR PILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 201-06-05
PRIOR FILING DATE: 201-06-05
PRIOR FILING DATE: 201-06-05
SOFTWARE: PATENTIN VOT: 2.1
SEQ. ID NO 60
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ORGANISM: Artificial sequence
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GENERAL INFORMATION:
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US-10-039-785-58
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220 AAGCGGGCCTCAGGGGTCTCTGTGGCTCCAAGTCTGGCAACACGGCCTCC 279
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Pred. No. 5.2e-68;
0; Mismatches 56;
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; OTHER INFORMATION: DNA encoding T1014B01 scFv
US-10-039-785-58
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR PILING DATE: 2001-08-02
PRIOR PILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 58
LENGTH: 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 67.0%;
Best Local Similarity 84.0%;
Matches 295; Conservative (
                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial sequence
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	December 29, 2003, 16:08:50 ; Search time 1615.57 Seconds (without alignments) 9875.644 Million cell updates/sec
Title: Perfect score:	US-09-019-441-1 390
Sequence:	1 ATGGCCTGGACTCTGCTCCTCCCGGTTGACCGTCCTAGGT 390
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2888711 segs, 20454813386 residues
Total number of	Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-arocessing: Minimum Match 0%

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : GenEmbl:\*
1: gb\_ba:\*
2: gb\_htg:\*

GenEmbl:\*

1: 9D ba:\*

2: 9D ba:\*

3: 9D ba:\*

4: 9D om:\*

4: 9D om:\*

5: 9D ow:\*

6: 9D ow:\*

7: 9D op:\*

10: 9D pat:\*

10: 9D pat:\*

10: 9D pat:\*

11: 9D pat:\*

11: 9D pat:\*

11: 9D pat:\*

12: 9D ow:\*

13: 9D ow:\*

14: 9D vi:\*

13: 9D vi:\*

14: 9D vi:\*

15: em pai:\*

16: em hum:\*

17: em hum:\*

18: em pai:\*

20: em ow:\*

21: em ov:\*

22: em pat:\*

22: em pat:\*

23: em pat:\*

24: em pat:\*

25: em pi:\*

26: em vi:\*

27: em vi:\*

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Pred. No. is the number of results predicted by chance to have a

em\_htgo\_hum:\* em\_htgo\_mus:\* em\_htgo\_other:\*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	ptio	343 H saniens	ORO Himan Id 1	139 Human Iq	33 H.sapiens	358 H.sapiens	035 H.sapiens	297 H.sapiens	355 H.sapiens	79222 Sequen	038 H.sapien	362 H.sapien	os4 H.Sapi	1000 1000 1100 1100 1100 1100 1100 110	33102 Homo san	032 H.sapiens	772 Human immu	029 H.sapie	18749 Homo	091 H.sapiens	295 H.sapiens	303 H.sapiens	125 H.sapiens	919 H. sapiens	ກໍເ	35365 Semience	Z85171 H.sapiens I	299 H.sapi	17851 Homo	823 Human	790 Hu	04760 Homo	197 H.sapien	296 H.sapiens	30983 Homo sap	924 H.sapiens	925 H.sapiens	030 H.sapiens	040 H.sapiens	031 H.sapiens	300 H.sapiens	926 H.sapiens	363 H.sapiens	359 H.sapiens	
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## ALIGNMENTS

	HSZ85043 435 DD DNA IINGAI PKI 06-FEB-1997	_	(24-17ITIIIH34) rearranged; Ig-Light-Lambda; VLambda.	Z85043	Z85043.1 GI:1834754	antigen receptor; immunoglobulin; immunoglobulin light chain;	immunoglobulin superfamily; rearranged; variable region.	Homo sapiens (human)		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1	Ignatovich, O., Tomlinson, I.M., Jones, P.T. and Winter, G.
RESULT 1 HSZ85043	rocus	DEFINITION		ACCESSION	VERSION	KEYWORDS		SOURCE	ORGANISM			REFERENCE	AUTHORS

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GGAAGAGGACCCGGTTGACCGTCCTAGGT 390
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/gene="IGL@"
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Matches 359; Conservative (
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Human Ig lambda L chain subgroup II V-2.DS mRNA, VJ region, partial
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L J. Mol. Biol.
CE 2 (bases 1 to 435)
RS Ignatovich, O.
NAL Bubmitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Location/Qualifiers
Location/Qualifiers
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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 Creation of Diversity in the Human Immunoglobulin V Lambda
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Pred. No. 1.4e-85;
0; Mismatches 31;
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Paul, E., Livneh, A., Manheimer-Lory, A. and Diamond, B. Characterization of the human immunoglobulin V-lambda-II gene family and analysis of V-lambda-II and C-lambda polymorphism in systemic lupus erythematosus J. Immunol. (1991) In press Location/Qualiflers
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                              HSZ85033 19 lambda light chain variable region gene (24-0/IIIIB176) rearranged; Ig-Light-Lambda; VLambda.
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Pred. No. 4e-85;
0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="peripheral blood"
/clone_lib="cDNA library"
                                                                                                                                                                                 419
                                                                                                                                          361 GGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
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Submitted (06-FEB-1997) Ignatovich
Engineering, Hills Road, Cambridge
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .435
/organism="Homo sapiens"
/mol type="genomic DNA"
/isolate="donor IT"
/db xref="taxon:9606"
/map="22q11.2"
                                                                                                                                                               390 GGGGAGGACCAAGCTGACGTCCTAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="24-07ITIIB176"
/cell_type="lymphocyte"
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/gene="IGLV"
1. .47
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/gene="IGLV"
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Best Local Similarity 91.8%;
Matches 358; Conservative
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J. Mol. Biol.
2 (bases 1 to 435)
Ignatovich,O.
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HSZ85033
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                                                                                  הטחביטטט 473 bp mRNA linear PRI 05-JAN-1995
Human Ig rearranged lambda chain (V-lambda-2.DS) mRNA, V-, J-, and
ברפקוסה subgroup II.
                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 473)

auth, E., Livroeh, A., Manheimer-Lory, A.J. and Diamond, B.
Characterization of the human Ig V lambda II gene family and analysis of V lambda II and C lambda polymorphism in systemic lupus
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                               M75119.1 GI:186154
C-region; J-region; V-region; immunoglobulin; immunoglobulin
lambda; immunoglobulin light chain; variable region subgroup II.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 ATGGCCTGGGCTCTGCTGCTCCTCACCCTCACTCAGGGCACAGGGTCCTGGGCCCAG
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Location/Qualifiers
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note="G00-128-432"
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/note="G00-128-432"
160 c 119 g 108 t
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/note="G00-128-432"
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ilarity 92.1%; Pred. No. 1.4e-85;
Conservative 0; Mismatches 31;
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92013092
      390 GGCGGAGGACCAAGCTGACCGTCCTAGGT 419
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/db_xref="taxon:9606"
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/note="leader; G00-128-432'
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/gene="IGL@"
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Best Local Similarity
Matches 359; Conservé
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PRI 06-FEB-1997
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                            241 GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG
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Direct Submission
Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen receptor; immunoglobulin; immunoglobulin light chain; immunoglobulin superfamily; rearranged; variable region. Homos sapiens (human)
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1.sapiens Ig lambda light chain variable region gene
124-09ITIIC195) rearranged; Ig-Light-Lambda; VLambda.
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/mol type="genomic DNA"
/isolate="denor IT"
/db xref="taxon:966"
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/clone="24-09ITIC195"
/cione="24-09ITIC195"
/tissue type="lymphocyte"
/tissue type="peripheral bl
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/gene="IGLV"
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/gene="IGLV"
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2 (bases 1 to 435)
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Matches 355; Conserv
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VERSION
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TITLE
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H.sapiens Ig lambda light chain variable region gene (25-28SWIID60)
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                                               241 AATGGTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 300
                                                                                                       GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTC 360
                                                                                                                          TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
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XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
Repertoire
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (06-FBB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 20H, UK
Location/Qualifiers
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antigen receptor; immunoglobulin; immunoglobulin light chain; immunoglobulin superfamily; rearranged; variable region.
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Homo sapiens
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/map="22q11.2"
/clone="52-288MIID60"
/cll_type="lymphocyte"
/tissue type="peripheral blood"
/clone_lib="cDNA library"
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/mol type="genomic DNA"
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/gene="IGLV"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (06-PEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
Location/Qualifiers
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antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
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Pred. No. 9.1e-84;
0; Mismatches 35; Indels
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/tissue_type="peripheral blood"
/clone_lib="cDNA library"
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/organism="Homo sapiens"
/mol type="genomic DNA"
/isoIate="donor SW"
/mb xref="texton:9606"
/map="22q1.2"
/clone="25-23SWIB16"
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Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 20H, UK
Location/Qualifiers
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/tissue_type="peripheral blood"
/clone_lib="cDNA library"
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Pred. No. 9.1e-84;
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/isolate="donor Ol at time
/db_xref="taxon:9606"
/map="22q11.2"
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llarity 91.0%;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
Location/Qualifiers
                                                                                                                                                                                                                         antigen receptor; immunoglobulin; immunoglobulin light chain; immunoglobulin superfamily; rearranged; variable region. Homo sapiens (human)
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H.sapiens Ig lambda light chain variable region gene
(24-12ITIIIE213) rearranged; Ig-Light-Lambda; VLambda
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/organism="Homo sapiens"
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/gene="IGLV"
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/gene="IGLV"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Compositions and methods for the therapy and diagnosis of colon
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CORIXA CORPORATION (US)
Location/Qualifiers
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/db_xref="taxon:9606"
198 c 154 g 128
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241 GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCTG 300
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                    GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTC
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Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
Location/Qualifiers
1. 435
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                  antigen receptor; immunoglobulin; immunoglobulin light chain; immunoglobulin superfamily; rearranged; variable region. Homo sapiens (human)
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H.sapiens Ig lambda light chain variable region gene
(24-08ITIIC194) rearranged; Ig-Light-Lambda; VLambda.
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// map="22q11.2"
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Pred. No. 2.1e-82;
0; Mismatches 38;
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/gene="IGLV"
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11 Similarity 90.3%;
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Ignatovich, O.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 20H, UK
Location/Qualifiers
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/tissue type="peripheral blood"
/clone lib="cDNA library"
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/isolate="donor SW"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (O6-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
Location/Qualifiers
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/db_xref="taxon:9606"
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/clone="25-36SWIF166"
/cell_type="peripheral blood"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Ignatovich, O.
Direct Submission
Submitted (G6-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
Location/Qualifiers
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/clone="25-315WIID182"
/tissue type="peripheral blood"
/clone_Tib="cona library"
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Pred. No. 2.1e-82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC033102 895 bp mRNA linear PRI 27-JUN-2002 Homo sapiens, Similar to immunoglobulin lambda joining 3, clone MGC:45681 IMAGE:4851128, mRNA, complete cds.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 895)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (15-UN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 43 Row: g Column: 22 This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction, Similarity but not identity to protein.
CCAGGCAAAGCCCCCCAAACTCATCATTTATGATGTCACTAAGCGGCCCTCAGGGGTCCCT
                                                                                                                     GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG
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/product="Similar to immunoglobulin lambda joining 3"
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/lab_host="DH10B-R"
/note="Vector: pOTB7"
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3C033102.1 GI:21619847
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DFYPGAVTVAWKADGSPVKAGVVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQV
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Job time : 1617.57 secs
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BF975970 880 bp mRNA linear EST 22-JAN-2001
602246174F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4337226 5',
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NIH-WGC http://mgc.noi.nih.gov/.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov.
Plate: LLCM1211 row: c column: 19
High quality sequence stop: 759.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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BG536723 602564852

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cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: NDAM388 row: k column: 08
High quality sequence stop: 885.
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0; Mismatches 35; Indels (
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                           Length 880;
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Conteat: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
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                                    organism="Homo sapiens"
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        location/Qualifiers
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Matches 358; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/cloon=lib="MIH MGC_48"
/cloon=lib="MIH MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXXhol sites using the Directionally cloned into EcoRIXXhol sites wising the following 5' adaptor: GGGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callfornia, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: Libis is a NIH—MGC_Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTGAGGACGAGGCTGATTATTACTGCAGCTCATATACAAGCAGCAGCACCTTGGGTATTC 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 recacregaaccaecaereacerreeraerraraaccerercereeraccaecaece 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 300
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 843)
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                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can k
found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLCM1705 row: b column: 10

High quality sequence stop: 838.
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Pred. No. 2.4e-78;
0; Mismatches 35; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="IMAGE:4855593"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
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ilarity 91.0%;
Conservative (
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Best Local
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ORIGIN
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/note="Torgan: spleen; Vector: pOTB7; Site_1: Xho1, Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/Xho1 sites using the following 5' adaptor: GGCACGA(GA). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
                     mRNA linear EST 12-MAR-2002 sapiens cDNA clone IMAGE:5480018
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2002 row: d column: 03
High quality sequence stop: 538.
I. 1078 Qualifiers

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1 (Dases 1 to 1078)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
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/mol_type="mRNA"
/db_xref="texcon:9606"
/clone="IMAGE:5480018"
/lab_host="DH108" (phage-resistant)"
/clone_lib="NIH_MGC_113"
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1078 bp
AGENCOURT 6615290 NIH MGC_113 Homo 15', mRNA sequence.
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BM914350.1 GI:19364729
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361 GGAAGAGGGACCCGGTTGACCGTCCTAGGT 390

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RESULT 4 BM914350 us-09-019-441-1.open.rst

VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

DEFINITION

RESULT 5 BX280395

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ACCESSION

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BI820758.1 GI:15932308
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Homo sapiens
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1 (bases 1 to 485)
Ebert, L., Heill, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.
Human UnigeneSet - RZPD3
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free from RZPD; contact RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares multiple_sclerosis 2NbHMSP"
/note="Vector: pT713D (Pharmacia) with a modified
polylinker V TYPE: phagemid; Site_1: Not I; Site_2: Bco I; let strand_cDNA was primed with a Not I - oligo(dT)
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Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; INAGD998E24628.
RZPDI.18; INAGD99E24628.
RZPDI.18; I.M.A.G. E. CDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/Cgi-
bin/showLib.pl.cgi/response7libNo-972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 111
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/mol_type="mRNA"
/db_xref="taxon:9606"
407 GGCGGAGGACCAAGCTGACGTCCTCGGT
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Best Local Similarity 90.5
Matches 353; Conservative
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FEATURES

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BASE COUNT ORIGIN

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/MOL type="mRNA"
// Ab Arref="taxon:9606"
// Clone="INAGE:175684"
/ lab host="MAGE:175684"
/ lab host="D4108"
// clone=lib="NIH MGC 115"
/ clone=lib="NIH MGC 115"
/ note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: Not!; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69: Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1:8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH MGC Library."
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
Tissue Procurement: Life Technologies, Inc.
Tobna Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov k column: 13
htgh quality sequence start: 2
High quality sequence stop: 785.
Location/Qualifiers
                                                                                                                                                                                                                                   181 CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT
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/organism="Homo sapiens"
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BG759257 686 bp mRNA linear EST 15-MAY-2001
602710936F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4851128 5',
mRNA sequence.
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for average insert size 1.8kb. Library constructed by Li Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Supersoript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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Fissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.go.

High quality sequence stop: 683.
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0; Mismatches 37; Indels 0;
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/db_xref="taxon:9606"
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Best Local Similarity 90.5%;
Matches 353; Conservative
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCMIG24 row: f column: 08
High quality sequence stop: 821.
                                                                                                                                                                                                                                                                            TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
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/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 48"
/note="Organ: B-cells, Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; conMa made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
11 (bases 1 to 829)
11H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (
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                    Length 787;
                Score 330.8; DB 12; Length
Pred. No. 1.7e-77;
0; Mismatches 37; Indels
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:4765447"
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                       84.8%;
90.5%;
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   Guery Match
Best Local Similarity 90.5'
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TITLE
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AV697043 GKC Homo sapiens cDNA clone GKCGWG01 5', mRNA sequence. AV697043
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1 (bases 1 to 767)

Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, O., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, H., Gu, J., Chen, Z. and Han, Z.

Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
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                                                                                                                                                                                                                                                                                                                                     /clone_lib="GKC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanz@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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                                                                                                                                                                               /organism="Homo sapiens"
/mol Lype="mkNa"
/mol Lype="mkNa"
/db xref="taxon:966"
/clone="GKCGWD05"
/tissus type="hopatocellular carcinoma"
/dev stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 329.2; DB 9;
Pred. No. 4.3e-77;
0; Mismatches 38;
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Best Local Similarity 90.3%;
Matches 352; Conservative (
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                        /tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone lib="NH MGC 48"
/note="Grgan: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGACAGGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is an MI MGC Library."
51 a 230 c 177 g 128 t
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AV693754 GKC Homo sapiens CDNA clone GKCGWD05 5', mRNA seguence.
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I bases 1 to 716)

Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, M., Shen, X., Lud, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Chen, Z. and Han, Z.

Insight into hepatocellular carcinogenegis at transcriptome level
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Chinese National Human Genome Center at Shanghai
                                                                                                                                                                                                                                                                                                                                                                                                         38;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 786)
NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                            /clone_lib="GKC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                              11752456
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
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 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
21625106
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                                                                                                                                                                                                                                                                                                                                                                                                  Length 767;
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                                                                                                                                                                                                                                                             /tissue type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                    This clone is available at CHGC in Shanghai
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                     DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 329.2; DB 9
Pred. No. 4.5e-77;
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                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GKCGWG01"
                                                                                                                                                                                                                                                                                                                                                       198 g
                                                                                                          Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                        Email: hanzg@chgc.sh.cn
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/Lissue_type="primary B-cells from tonsils (cell line)"
/lab host="primary B-cells from tonsils (cell line)"
/lab host="primary B-cells from tonsils (cell line)"
/clone_lib="NIH MGC 48"
/clone_lib="NIH MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: Xho1;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/Xho1 sites using the following 5' adaptor: GGCAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscribt II RT (Life Technologies).
Note: this is a NIH MGC Library."
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Plate: LLCM1699 row: i column: 03
High quality sequence stop: 786.

1. 786
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 4.5e-77;
0; Mismatches 38;
                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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/ db_xref="taxon:9606"
/ clone="InAGE-485399"
/ tlssue type="primary B-cells from tonsils (cell line)"
/ lab_host="DH10B (phage-resistant)"
/ lab_host="DH10B (phage-resistant)"
/ clone libe-mNHH MGC 48"
/ note="Organ: B-cells; vector: pOTB7; Site 1: Xho1;
Site 2: ECOR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1XXhol sites using the following 5' adaptor: GGCAGAG(G). Size-selected 550bp for average insert aize 1.8kb. Library constructed by Ling Hong in the labbratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscribt II RT (Life Technologies).
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                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Inorthe Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1700 row: 1 column: 16
High quality sequence stop: 810.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 4.8e-77;
0; Mismatches 38; Indels
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                                                              Homo sapiens (human)
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602710363F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4850871 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Upposition Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Glone distribution information can be
found through the I.M.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLCM1692 row: m column: 16

High quality sequence stop: 885.
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1 (bases 1 to 908)
11 "Mt-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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90.3%; Pred. No. 4.8e-77;
iive 0; Mismatches 38
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH_MGC-48"
/note="Crgan: B-cells; Vector: pOTB7; Site_1: KhoI;
Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into ECORI/KhoI sites using the following 5; adaptor: GGCAGGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Supersoript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                              Contract: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tisaue Procurement: Louis M. Staudt, M.D., Ph.D.
Tisaue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1282 row: k column: 21
High quality sequence stop: 881.
Location/Qualifiers
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 980)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                          213 CCAGGCAAAGCCCCCAAACTCATGATTTATGAGGTCAATAAGCGGCCCTCAGGGGTCCCT
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ilarity 90.3%; Pred. No. 5e-77;
Conservative 0; Mismatches 38;
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:4565516"
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/clone_llb="NH1MGC_48"
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Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1X/Xho1 sites using the Directionally cloned into EcoR1X/Xho1 sites asing the following 5' adaptor: GGGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
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602245104P1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4336177 5',
mRNA sequence.
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       GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTC 360
                                            TGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC 180
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCML208 row: h column: 02
High quality sequence stop: 777.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tsaue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                           361 GGAAGAGGACCCGGTTGACCGTCCTAGGT 390
                                                                                                                                                                                    GGCGGAGGACCAAGCTGACCGTCCTAGGT 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:4336177"
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/db_xref="taxon:9606"
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TITLE
JOURNAL
COMMENT
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KEYWORDS
SOURCE
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Search completed: December 29, 2003, 21:44:05 Job time : 1691.58 secs

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Sequence Sequence

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64, Appl 4, Appli 16554, A 54, Appl 54, Appl

Sequence Sequence 18093, A 18093, A 15053, A 57, Appl

Sequence

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Sequence Sequence

Version #1.30

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Result

TELEFAX: (703) 836-INFORMATION FOR SEQ ID NO: 1:

Sequence 2 Sequence 2

Title:

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KLOETZER, William S.
NAKAMURA, Takehiko
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
ANTIBODIES AND USE THEREOF AS THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
STREET: P.O. Box 1404
US-10-198-053-267
US-09-918-95-16199
US-09-191-35-146
US-00-139-785-64
US-10-139-785-64
US-10-139-785-64
US-10-039-785-64
US-10-039-785-64
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US-10-139-785-60
US-10-032-386-436
US-10-139-785-59
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CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTINE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,441
FILING DATE: 05-Feb-1998
CLASSIFFICATION: «Unknown»
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FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, RObin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
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TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09019441 Publication No. US20030086921A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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Sequence 13540, A
Sequence 36573, A
Sequence 16692, A
Sequence 8, Appli
Sequence 13, Appli
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Sequence 13, Appl
Sequence 13540, A
Sequence 16500, A
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Sequence 1, Appli
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2371.523 Million cell updates/sec
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390
1 ATGGCCTGGACTCTGCTCCT......CCCGGTTGACCGTCCTAGGT 390
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Sequence 2
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| cgn2 \( \frac{7}{2} \) prodata/2/pubpna/USO7 \( \text{PUBCOMB. eeq:*} \) | cgn2 \( \frac{7}{2} \) prodata/2/pubpna/PCT \( \text{NEW PUB. eeq:*} \) | cgn2 \( \frac{6}{2} \) prodata/2/pubpna/PCT \( \text{NEW PUB. eeq:*} \) | cgn2 \( \frac{6}{2} \) prodata/2/pubpna/USO6 \( \text{NEW PUB. eeq:*} \) | cgn2 \( \frac{6}{2} \) prodata/2/pubpna/USO6 \( \text{NEW PUB. eeq:*} \) | cgn2 \( \frac{6}{2} \) prodata/2/pubpna/USO6 \( \text{NEW PUB. eeq:*} \) | cgn2 \( \frac{6}{2} \) prodata/2/pubpna/USO9 \( \text{NEW PUB. eeq:*} \) | cgn2 \( \frac{6}{2} \) prodata/2/pubpna/USO9 \( \text{NEW PUB. eeq:*} \) | cgn2 \( \frac{6}{2} \) prodata/2/pubpna/USO9 \( \text{PUBCOMB. eeq:*} \) | cgn2 \( \frac{6}{2} \) prodata/2/pubpna/USO9 \( \text{PUBCOMB. eeq:*} \) | 11: \( \frac{6}{2} \) \( \frac{6}{2} \) prodata/2/pubpna/USO9 \( \text{PUBCOMB. eeq:*} \) | 12: \( \frac{6}{2} \) \( \frac{6}{2} \) prodata/2/pubpna/USO9 \( \text{NEW PUB. eeq:*} \) | 13: \( \frac{6}{2} \) \( \frac{6}{2} \) prodata/2/pubpna/USO9 \( \text{NEW PUB. eeq:*} \) | 14: \( \frac{6}{2} \) \( \frac{6}{2} \) prodata/2/pubpna/USO9 \( \text{NEW PUB. eeq:*} \) | 15: \( \frac{6}{2} \) \( \frac{6}{2} \) prodata/2/pubpna/USO9 \( \text{NEW PUB. eeq:*} \) | 16: \( \frac{6}{2} \) \( \frac{6}{2} \) prodata/2/pubpna/USO9 \( \text{NEW PUB. eeq:*} \) | 16: \( \frac{6}{2} \) \( \frac{6}{2} \) \( \text{PUBCOMB. eeq:*} \) | 17: \( \frac{6}{2} \) \( \text{PUBCOMB. eeq:*} \) | 17: \( \frac{6}{2} \) \( \text{PUBCOMB. eeq:*} \) | 17: \( \frac{6}{2} \) \( \text{PUBCOMB. eeq:*} \) | 17: \( \frac{6}{2} \) \( \text{PUBCOMB. eeq:*} \) | 17: \( \frac{6}{2} \) \( \text{PUBCOMB. eeq:*} \) | 17: \( \frac{6}{2} \) \( \text{PUBCOMB. eeq:*} \) | 17: \( \frac{6}{2} \) \( \text{PUBCOMB. eeq:*} \) | 17: \( \frac{6}{2} \) \( \text{PUBCOMB. eeq:*} \) | 17: \( \frac{6}{2} \) \( \text{PUBCOMB. eeq:*} \) | 17: \( \frac{6}{2} \) \( \text{PUBCOMB. eeq:*} \) | 17: \( \frac{6}{2} \) \( \text{PUBCOMB. eeq:*} \) | 17: \( \frac{6} \) \( \text{PUBCOMB. eeq:*} \) | 17: \( \frac{6} \) \( \t
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                          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-103-686-1
US-10-198-846-13206
US-10-198-846-13540
US-09-918-995-16692
US-10-076-747-8
US-10-076-13540
US-10-125-108A-13
US-10-198-846-13540
US-10-158-646-76
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US-09-907-969-267
US-09-827-271-267
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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FILING DATE: 25-Mar-2002
CLASSIFICATION: <Unknown>
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RPELICANT: REFF, Milliam S.
NAKAMURA, Takehiko.
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
ANTIBODIES AND USE THEREOF AS THERAPEUTICS
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
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ADDRESSES: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                 100.0%; Score 390; DB 11;
100.0%; Pred. No. 6.1e-118;
iive 0; Mismatches 0;
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APPLICATION NUMBER: US/10/103,686
                                                                                                                                                                                              LOCATION: 58.7390
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1, Application US/10103686
; Publication No. US20030059424A1
; GENERAL INFORMATION:
                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
             LENGTH: 390 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Virginia
COUNTRY: United States
                                                                                                                                                                           NAME/KEY: mat_peptide
 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 35
                                                                                                                                         1..390
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Best Local Similarity 100.
Matches 390; Conservative
                                                                                                                         NAME/KEY:
                                                                                                                                         LOCATION:
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US-10-103-686-1
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Publication No. US200309974A1
Publication No. US200309974A1
APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OP INVENTION: THERAPY OF BREAST CANCER
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; Pred. No. 6.1e-118;
0; Mismatches 0;
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RABISTRATION NUMBER: 35,030

REPERBNCE/DOCKET NUMBER: 012712-353

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
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US-10-103-686-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mat_peptide
58..390
                                                                                                                                                                                                                                                                                                                      LENGTH: 390 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.0
Matches 390; Conservative
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; Sequence 36573, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
    APPLICANT: Hyseq, Inc.
    TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
    CURRENT APPLICATION NUMBER: US/09/218,995
    CURRENT FILING DATE: 2001-07-30
    PRIOR FILING DATE: 1999-01-20
    NUMBER OF SEQ ID NOS: 38054
    SOF THARE: FeastSEQ for Windows Version 3.0
    SEQ ID NO 36573
    LENGTH: 408
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Pred. No. 2.3e-96;
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Mismatches
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Best Local Similarity 89.5%;
Matches 349; Conservative
    350; Conservative
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US-09-918-995-36573
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PREVENTION, AND
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| Publication No. US2003009974A1
| GENERAL INFORMATION:
| APPLICANT: LILIGH. James
| APPLICANT: LILIGH. James
| APPLICANT: LILIGH. James
| APPLICANT: Steinmann, Kalbien
| TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREV
| TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREV
| FILE REFERENCE: MRI-049
| CURRENT APPLICATION NUMBER: US/10/198,846
| CURRENT FILING DATE: 2002-07-18
| PRIOR PILING DATE: 2001-07-18
| NUMBER OF SEQ ID NOS: 14084
| SEQ ID NO 13540
| LENGTH: 1597
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Pred. No. 7e-97;
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FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
FRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13206
LENGTH: 1640
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90.0%;
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Best Local Similarity 90.0%;
Matches 351; Conservative
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Best Local Similarity
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; ORGANISM: Homo E
US-10-198-846-13206
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259 AATGGCTTCTGGGTTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 318
                                                 GCTGAGGACGAGGCTGATTATTACTGTTGTTATACAACCAGTAGCACTTTGTTATTC 360
                                                                      319 GCTGAGGACGAGGCTCATTATTATTGCAGTTCATATACAACCAGAAGCACTCTCGTCTTC 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41; Indels
                                                                                                                                                                                                                             Sequence 16692, Application US/09918995
Publication No. US2003007362341
GENERAL INFORMATION:
APPLICANT: Hyeeq. Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
FILE REFERENCE: 20411-756
CURRENT PAPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR PHING DATE: 1999-01-20
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89.5%; Pred. No. 2.3e-96;
iive 0; Mismatches 41
                                                                                                                   361 GGAAGAGGACCCGGTTGACCGTCCTAGGT 390
                                                                                                                                         GGAAATGGGGCCAAGGTCACCGTCCTATGT 408
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16692
LENGTH: 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 89.5
Matches 349; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-16692
                                                                                                                                                                                                      RESULT 6
US-09-918-995-16692
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Sequence 8, Application US/10076747
Publication No. US20030180726A1
GENERAL INFORMATION
APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto

US-10-076-747-8

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APPLICANT: Karra, Kabana
APPLICANT: Karra, Kabana
APPLICANT: Gafferkey, Robert
APPLICANT: Gafferkey, Robert
APPLICANT: Gun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Ovarian Specific Genes and P)
FILE REFERENCE: DRX-0315
CURRENT APPLICATION NUMBER: 18/10/076,747
CURRENT APPLICATION NUMBER: 60/268,290
PRIOR FILING DATE: 2001-02-13
PRIOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 129
SOTWARE: Patentin version 3.1
SEQ ID NO 8
FROM FILENCE OF SEQ ID NOS: 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 CACTGGAACCAGCAGTCACGTTGGTGATATAACTATGTCTCCTGGTACAACAACACCACC 180
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Publication No. US20030157112A1
GENERAL INFORMATION:
APPLICANT: HOOPER, Craig
APPLICANT: DIETZSCHOLD, Bernhard
TITLE OF INVENTION: Recombinant Antibodies, and Compositions
TITLE OF INVENTION: and Methods for Making Them
FILE REPERBNCE: 93121-110
CURRENT FILING DATE: 2003-04-10
FRIOR APPLICATION NUMBER: US/10/225,108A
CURRENT FILING DATE: 2003-04-10
PRIOR PILING DATE: 2001-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 322.4; DB 13
Pred. No. 1.6e-95;
0; Mismatches 41;
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LOCATION: (1022)..(1022)
OTHER INFORMATION: a, c, g or
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Best Local Similarity 89.4%;
Matches 347; Conservative
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ORGANISM: Homo sapien
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US-09-918-995-16500
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PREVENTION, AND
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                                                                                                                                                                                Length 726;
                                                                                                                                                                                Score 313.2; DB 13; Length
Pred. No. 1.4e-92;
0; Mismatches 38; Indels
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Sequence 135-0.7

Publication No. US2003009974a1

GENERAL INPORMATION:

APPLICANT: Xu, Yongyao

APPLICANT: Xu, Yongyao

APPLICANT: Wang, Youthen

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND

TITLE OF INVENTION: THERAPY OF BREAST CANCER

FILE REFERENCE: MRI-049

CURRENT FAPLICATION NUMBER: US/10/198,846

CURRENT FILING DATE: 2002-07-18

PRIOR FILING DATE: 2001-07-18

PRIOR FILING DATE: 2001-07-18

NUMBER OF SEQ ID NOS: 14064

SOFTWARE: FREESEQ for Windows Version 4.0

LEMATH: 15-0
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88.9%; Pred. No. 1.8e-92;
iive 0; Mismatches 38;
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PRIOR APPLICATION NUMBER: US 60/204,518
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: US 60/314,023
PRIOR FILING DATE: 2001-08-21
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 13
                                                                                                                                                                                  88.9%;
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Best Local Similarity 88.5
Matches 352; Conservative
                                                                                                                                                                                                Best Local Similarity 88.5
Matches 352, Conservative
                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-10-198-846-13540
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                                                                                                                                                      US-10-225-108A-13
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                                           35 ATGGCCTCTGGCTGCTCCTCACCCTCCTCACTCAGGGCACAGGGTCCTGGGCCCAG
                                                                                                                              61 TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC
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; Publication No. US20030073623A1
; GENERAL INFORMATION:
    APPLICANT: Hyseq, Inc.
    TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
    TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
    TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
    FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastESQ for Windows Version 3.0
; SEQ ID NO 16500
; LENGTH: 420
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US-09-884-441-267
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265 AATCGCTTCTCGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGGCTCCAG 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030073105A1 1329913.2
US-10-158-646-73
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Foundation No. US20030073105A1
GENERAL INFORMATION:
APPLICANT: Lasek, Amy K.W.
TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
FILE REFERENCE: PA-0030-1 US
CURRENT APPLICATION NUMBER: US/10/158,646
CURRENT APPLICATION NUMBER: 0202-05-29
FRIOR PILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PERL PROGRAM
SEQ ID NOS: 78
LENGTH: 983
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US-10-158-646-73
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RESULT 12
US-10-158-646-76/C
'Sequence 76, Application US/10158646
'Publication No. US20030073105A1
'GENERAL INFORMATION:

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Post Local Similarity 87.2%; Pred. No. 3e-88;
Matches 341; Conservative 0; Mismatches 49; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030073105A1 1329881.6
US-10-158-646-76
        TITLE OF INTENTION: GENES EXPRESSED IN COLON CANCER; FILE OF INTENTION: GENES EXPRESSED IN COLON CANCER; FILE REPERENCE: PA-0030-1 US; CURRENT APPLICATION NUMBER: US/10/158,646; CURRENT FILING DATE: 2002-05-29; PRIOR APPLICATION NUMBER: 60/295,239; PRIOR FILING DATE: 2001-05-31; NUMBER OF SEQ ID NOS: 78; SOFTWARE: PERL Program

SEQ ID NO 76; LENGTH: 2667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 267, Application US/0988441
; Sequence 267, Application US/0988441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
    APPLICANT: Adgate, Paul A.; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER; FILE REFERENCE: 210121.4627.
; CURRENT PELLING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 267
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Sornasse, Thierry
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NAME/KEY: misc_feature
LOCATION: (1)...(548)
                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapien
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121 TGCACTGGAACCAGGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC 180
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                         47 ATGGCCTGGGCTCTCCTCCTCCTCCTCCTCCTCAGGCACAGGCTCCTGGGCCCAG
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CCTCGTCACCCTCCTCACTCAGGGCACAGGATCCTGGGCTCAG
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Fublication No. US20030165504A1
GENERAL INFORMATION:
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER;
FILE REFERENCE: 210121.462C6;
CURRENT PAPLICATION NUMBER: US/09/827,271
CURRENT PAPLICATION NUMBER: US/09/827,271
CURRENT PILING DATE: 2001-04-04
NUMBER OF SEQ ID NOS: 461
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 267
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// LOCATION: (1)...(548)
// OTHER INFORMATION: n = A,T,C or G
US-09-827-271-267
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ORGANISM: Homo sapien
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JAPPLICANT: Mincham, Jennifer L.
APPLICANT: King, Gordon E.
JAPPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Retter, Marc M.
JAPPLICANT: Reed, Steven P.
APPLICANT: Reed, Steven G.
APPLICANT: Albone, Earl
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
TITLE REFERENCE: 21012.1.46208
CURRENT FILING DATE: 2001-07-17
NUMBER OF SEG ID NOS: 596
SOFTMARE: FastESQ for Windows Version 4.0
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                                                                                                  46; Indels
                                                        Score 295.2; DB 10;
Pred. No. 1e-86;
0; Mismatches 46;
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; LOCATION: 346, 358, 432, 510, 512
OTHER INFORMATION: n = A,T,C or G
US-09-907-969-267
    or
  = A, T, C
                                                          Query Match 75.7%;
Best Local Similarity 87.7%;
Matches 343; Conservative
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ORGANISM: Homo sapiens
  OTHER INFORMATION: n
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US-09-907-969-267
    ; OTHER INFURM
US-09-884-441-267
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120

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286

us-09-019-441-1.open.rnpb

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        Qy
        241 GATCGCTTCTCGCTCCAAGTCTGGCAACACGCCTCCTGACCATCTCTGGGCTCCAG 300

        Db
        287 GATCGCTTCTCTGCTCCAAGTCTGGCAACACGCCTCCCTGACCGTCTCTGGGGTCCAN 346

        Qy
        301 GCTGAGGACGAGGCTGATTATTACT-GTTGTTCATATACAACCAGTAGCACTTTGTTATT 359

        Db
        347 GCTGAGGATGATATTACTGGAAGCTCATATGCAGCACAACAATTGGGTGTT 406

        Qy
        360 CGGAAG-AGGGACCGGTTGACCTTGGGAAGCACAACAATTGGGTGTT 406

        Db
        407 CGGCGGAAGGGACCAAGCTGACCGTNCTAAG 437
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Search completed: December 30, 2003, 03:42:07 Job time : 565.449 secs

Mouse DNA encoding DNA encoding throm DNA encoding novel DNA encoding novel Human prostate exp Human prostate exp DNA encoding novel DNA encoding novel

Human prostate exp Human prostate exp Human autoantibody Nucleotide sequenc Nucleotide sequenc MH4H7 Mab light ch Variable region of

Human ovarian carc Ovarian carcinoma DNA encoding anti Nucleotide sequenc Nucleotide sequenc Human U266 lambda

U266-Lambda gene a

Human autoantibody APRIL binding scFv Recombinant human

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DNA encoding throm
Mouse DNA encoding
Thrombopoietin (TP

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Anti-human CD23 6G5 monoclonal antibody light chain variable region DNA.
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AAS83483
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ABV77130
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AAQ36134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | SIDSI/goddata/geneseq/geneseqn-embl/NA1981.DAT:
| SIDSI/goddata/geneseq/geneseqn-embl/NA1981.DAT:
| SIDSI/goddata/geneseqn-embl/NA1981.DAT:
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| SIDSI/goddata/geneseq/geneseqn-embl/NA1991.DAT:
| SIDSI/goddata/geneseq/geneseqn-embl/NA1999.DAT:
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1 ATGGCCTGGACTCTGCTCCT......CCCGGTTGACCGTCCTAGGT 390
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/geneseqn-embl/NA2001B.DAT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Geneseq 19Jun03:*
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.
                    GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                            2552756 seqs, 1349719017 residues
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                                                                                                                                                  December 29, 2003, 16:08:50
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Maximum Match 100%
Listing first 45 summaries
                                                                                                           nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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DB seq length: 200000000
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322.4 321.2 319.6 316.4 313.6

Score

Result

Post-processing:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chain variable region of primate monoclonal antibody anti-human CD23 6G5. The invention provides primate monoclonal antibody anti-human CD23. The invention provides primate monoclonal antibodies which specifically bind human CD23, the low affinity receptor for IgE (FeeRii/CD23), and comprise either of a human gamma-1 or human gamma-3 constant region that binds to human Fc gamma receptors and inhibits IgE expression. The monoclonal antibodies of the invention are claimed to be useful for inhibiting induced IgE production for treating or preventing allergic, inflammatory and autoimmune conditions e.g. allergic rhinitis conjunctivitis, autoimmune hamenlytic anaemia, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present sequence represents a DNA sequence encoding the light
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               /*tag= e
/note= "encodes CDR 2 region"
328..357
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/note= "encodes CDR 3 region"
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98US-0019441.
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211..231
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(SEGK ) SEIKAGAKU CORP
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Best Local Similarity
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misc_feature
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05-FEB-1998;
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The invention relates to an isolated polynucleotide (I) encoding a polypeptide (II) comprising a portion of a colon tumour protein. A new colsymbotide (III) that bybridises to (I) is useful for determining the presence of a cancer in a patient. (II) or antigen presenting cells specific for a tumour protein, by contacting T cells of antigen. The specific for a tumour protein, by contacting T cells of antigen presenting cells that express (II) are useful for treating or antigen presenting cells that express (II) are useful for treating or antigen presenting cells that express (II). (II), or antigen presenting cells that express (II) so that T cells proliferate, and administering to the patient and from a patient of the proliferated T cells, thus inhibiting the cancer in the patient. A new composition is useful in development of a cancer in the patient. (I) or (II) is useful in cancer and for the diagnosis in a patient. (I) or (II) is useful in colon cancer and for the diagnosis and monitoring of the cancers. (I), (II) or an antibody against (II) is useful as a probe or primer for nucleic acid hybridisation, and in the design and preparation of ribozyme molecules for inhibiting expression of (II) in tumour calls. ABK29475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TCTGCCCCGACTCAGCCTCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
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Pred. No. 2.9e-92;
0; Mismatches 35; Indels (
                                                                                                                                                                                                                                     88.
                                                                                                                                                                                                                                   Human; colon adenocarcinoma; colon cancer; tumour; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 605 BP; 123 A; 198 C; 154 G; 128 T; 2 other;
Secrist H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide encoding a pof colon tumour protein, for detection,
                                                                                                                                                                                                    Colon adenocarcinoma-specific cDNA #264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 181-182; 211pp; English
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                                                                                                    ABK29738 standard; cDNA; 605
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ilarity 91.0%;
Conservative
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22-NOV-2000; 2000US-252614P.
                                                                                                                                                                                                                                                                                                                                                                     07-JUN-2001; 2001WO-US18574
                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Meagher MJ, King GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-098052/13.
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Best Local Similarity
Matches 355; Conserv
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                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                     23-APR-2002
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                                                                                                                                      ABK29738;
                                                                     RESULT 2
ABK29738
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WPI; 2001-030926/04
P-PSDB; AAB63212.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a new isolated nucleic acid termed ovarian specific nucleic acid (OSNA) comprising: (a) a nucleic acid molecule that encodes any of 51 fully defined protein sequences appearing as ABUG1018-ABUG1070 (termed ovarian specific proteins, OSP); (b) any of 76 fully defined nucleotide sequences appearing as ABX92187-ABX92262; or (c) a sequence having at least 60% sequence identity to the nucleic acid molecule of (a) or (b). Also included are a method for determining the presence of an ovary specific nucleic acid (OSNA) in a sample, a vector comprising an OSNA, a host cell comprising the vector, an isolated OSP polypeptide, an anti-OSP antibody or fragment,
TCTGCCCTGACTCAGCCTCCCTGGTCTGGGTCTCCTGGACAGTCGACCATCTCC 152
                                                       212
                                                                             240
                                                                                                    272
                                                                                                                                      AATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAA 332
                                                                                                                                                                                   241 GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 300
                                                                                                                                                                      GCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTATTC 360
                                                                                          CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCACTAGTCGGCCCTCAGGGTTTCT
                                                      TGCACTGGAACCAGCAGTGACGTTGGTGGTTATAACCATGTCTCCTGGTACCAACAACAC
                                                                             CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT
                                                                                                                                                                                                                                                                                                                                                                                      Human, gene, 88; ovarian specific nucleic acid; OSNA, ovarian cancer, non-cancerous ovarian disease; gene therapy; vaccine; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated OSNA nucleic acid and encoded polypeptide, useful for identifying, diagnosing, monitoring, staging, imaging and treating ovarian cancer and non-cancerous diseases in ovarian tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cafferkey R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hu P, Recipon H, Karra K,
                                                                                                                                                                                                                                                                                                                                                                 Human ovarian specific nucleic acid DEX0310_8.
                                                                                                                                                                                                                   GGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
                                                                                                                                                                                                                                 GCGGAGGACCAAGGTGACCGTCCTAGGT 422
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15-FEB-2001; 2001US-268834P.
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                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salceda S, Macina RA,
Sun Y, Liu C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 CACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCACC 182
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a method for determining the presence of an ovary specific protein in a sample and a vaccine comprising an OSP or OSNA. The methods and compositions of the present invention are useful for identifying, diagnosing, monitoring, staging, imaging and treating ovarian cancer non-cancerous disease in ovary tissue. The present sequence is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 322.4; DB 29
Pred. No. 1.5e-88;
0; Mismatches 41
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Best Local Similarity 89.4%;
Matches 347; Conservative
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New human immune system associated proteins (HISAP) and polynucleotides encoding the HISAP, useful for diagnosing, treating or preventing immune or cell proliferative disorders or infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 891;
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89.0%; Pred. No. 2.8e-88;
ive 0; Mismatches 43
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                                                                                                                                        Claim 3; Column 87-90; 54pp; English
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Matches 347; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.9%; Score 319.6; DB 14; Length 902; 88.7%; Pred. No. 8.8e-88; ive 0; Mismatches 44; Indels 0;
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/label= C lambda
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/label= CDR3
389..421
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91GB-0016594.
92GB-0006284.
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/label= CDR1
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          /label= FF
155..196
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853..858
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Matches 346; Conservative
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23-MAR-1992;
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                                                                                                                                                                                                                                                                                                                       GCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTATTC 360
                                                                             TGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC 180
                                                                                                                                                          CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mapping; gene mapping; gene therapy; forensic;
medical imaging; diagnostic; genetic disorder;
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2000US-0649167.
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P-PSDB; ABG12886.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGGCCTGGACTCTGCTCCTCGTCACCCTCCACGGCCACAGGATCCTGGGCTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                           Sequence 889 BP; 200 A; 293 C; 223 G; 173 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46;
                                                                                                                                                                                                                                                                                                                                                                                                                  81.1%; Score 316.4; DB 2.88.2%; Pred. No. 8.3e-87; ive 0; Mismatches 46
                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
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2000US-0649167.
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Matches 344; Conservative
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Human; gene; ds; antibody; constant region; monoclonal antibody 57; Mab 57; variable region; Rabies; neurological disease; infection; central nervous system; rabies virus; Lyssavirus; Rhabdoviridae; pathogen; vaccine; virucide; light chain.

(UYJE-) UNIV JEFFERSON THOMAS

21-AUG-2002; 2002WO-US26584. 21-AUG-2001; 2001US-314023P.

WO2003016501-A2.

27-FEB-2003

Homo sapiens

monoclonal rabies virus antibody light chain, clone 57

(first entry)

10-MAY-2003

encoding

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAGGCAAAGCCCCCCAAAATCATGATTATGAGGTCAGTAAGCGGCCCTCAGGGGTTTCT
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                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 80.4%; Score 313.6; DB 23; Length Best Local Similarity 89.1%; Pred. No. 5.7e-86; Matches 351; Conservative 0; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 763 BP; 173 A; 242 C; 202 G; 146 T; 0 other;
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                                                                                                                                                                                                                 Claim 1; SEQ ID No 19284; 103pp; English.
Tang YT;
                                        2001-639362/73
Liu C,
Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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The invention discloses a recombinant antibody comprising a constant region of monoclonal antibody (Mab) 57 linked to a non-Mab 57 variable region. Rabies is an acute, neurological disease caused by infection of the creatural nervous system with the rabies virus, a member of the C. Vassavirus genus of the family Rhabdoviridae. Also disclosed are methods for producing an isolated recombinant antibody by culturing a host cell, containing a recombinant expression vector comprising the nucleic acid molecule encoding the antibody, and isolating the recombinant antibody administering to the individual exposed to a pathogen by administering to the individual the recombinant antibodies are useful for preventing (vaccine) and treating an individual cantibodies are useful for preventing (vaccine) and treating an individual the recombinant antibodies are useful for preventing (vaccine) and treating an individual called exposed to a pathogen, e.g. rabies infection. They are also useful for the qualitative and quantitative determination of the rabies virus. The sequences presented are the antibody protein fragments, the nucleic acids encoding them or the PCR primers used to construct the recombinant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant antibody comprising a constant region of Mab 57 linked to a non-Mab 57 variable region, useful for treating an individual exposed to a pathogen, e.g. rabies infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TECACTGGAACCAGCAGTGATATTGGTGGTTATAACTTTGTTCTCCTGGTACCAACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 36-37; 38pp; English
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Best Local Similarity
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ABX12863 standard; DNA; 726

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Sequence 448 BP; 89 A; 142 C; 113 G; 104 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, colyperates chain reaction (FCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques contour contour activity of (II) or to treat disease states involving contour and activity of (II) or to treat disease states involving contour and applying partners are useful in medical captor and properties in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical calsorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in captor diagnostics, forensics, gene mapping, identification of mutations captor general sequences of the invention.

Contour contour contour captor captor captor traits to assess biodiversity and to produce other types of data and products dependent on DNA and captor contour sequences. AAS64197-AAS94564 represent novel human captor data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO captors.
               GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 315
                                                    354
                                                                       GCTGAGGATGAGGCTGATTATTACTGCTGCTCATATGCAGGCGACTACACCCCGGGCGTG 375
GATCGCTTCTCTCGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG
                                                  GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCAC-----TTTG
                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                           DNA encoding novel human diagnostic protein #12874
                                                                                                      TTATTCGGAAGAGGACCCGGTTGACCGTCCTAGGT 390
                                                                                                                      376 GTTTTCGGCGGAGGACCAAGCTGACGTCCTAGGT 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID No 12874; 103pp; English.
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                    (first entry)
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P-PSDB; ABG12883.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGAGGACGAGGCTGATTATTACTGCTGCTCATATGCAGGTAGTAGCACTTATGTCTTC 407
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                                                                                                                                                                                                                                                                                          108 TCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                         recacregaaccaecagrearerregaaarraraaccrrercregrecracaacaecac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT
                                                                                                                  1 ATGGCCTGGACTCTGCTCCTCGTCACCCTCACTCAGGGCACAGGATCCTGGGCTCAG
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Flt-3 ligand; Fms-like tyrosine kinase; mouse; human; vaccine; immunotherapy; therapy; tumour; lymphoma; gene therapy; VR1642; plasmid VAXID; antibody; idiotype; vector; ss.
                                                            ö
79.5%; Score 310; DB 23; Length 448; 87.2%; Pred. No. 5.9e-85; tive 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAAGAGGACCCGGTTGACCGTCCTAGGT 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bicistronic idiotype plasmid VR1642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF30316 standard; cDNA; 7528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        c - Cytomegalovirus.
c - Mus musculus.
c - Homo sapiens.
c - Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JUL-2000; 2000WO-US20679.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                         Conservative
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                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200109303-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hermanson GG;
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Tsunoda H;

셤 ò 요 ð g ò 셤 ò g ઠે 셤 ò

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The invention relates to a new modified single chain FV antibody containing at least two Heavy chain variable domains and at least two light chain variable domains from the same or different monoclonal antibodies and which is an agonist for crosslinking a molecule at the cell surface or within the cell and thereby transducing a signal into the mirror and the interpretation of the antibodies by culture of the transformed cells, drug compositions the antibodies by culture of the transformed cells, drug compositions containing the antibodies and an assay method for the agonist activity of the antibodies by contacting the antibodies with cells expressing the relevant cell surface or internal molecule. The antibodies are useful for treatment and prevention of cancer, inflammatory disease, hormonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 AATGGTTCTGTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATGTGCTGACTCAGCCACCCTCGGTGTCAGGGTCTCCTGGACAGTCGATCACCATCTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 recacresaaccascasreacertesresranaacrarerecresraceaacascac 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Areaccracaccrrcrccrccaccrcrcrcrcrcrcacaccrcraaaccrcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGGCCTGGACTCTGCTCCTCGTCACCTCACTCAGGCCACAGGATCCTGGGCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified single chain multimeric Fv antibody acting as a signal transduction agonist for treatment of inflammatory hormonal and blood disorders and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rereceedacresecrecererereresegrerecresaças acadeses rerecentes rereces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence encoding an antibody of the invention or a fragment thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorders including diabetes, autoimmune disease, leukaemia, dysendocrinism and blood disorders. The present sequence is a DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.7%; Score 307; DB 24; Length 387; Larity 87.1%; Pred. No. 4.6e-84; Conservative 0; Mismatches 50; Indels (
                                                                                                                                                                                                                                                                         Yabuta N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 387 BP; 79 A; 124 C; 95 G; 89 T; 0 other;
                                                                                                                                                                                                                                                                         Ohtomo T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 8; Page 205-206; 217pp; Japanese.
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                                                                                                                                                                                                                                                                             Uno S,
                     20-OCT-2000; 2000JP-0321822.
12-MAR-2001; 2001WO-JP01912.
17-APR-2001; 2001WO-JP03288.
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                                                                                                                                      2001JP-0277314
                                                                                                                                                                                                                                                                             Tsuchiya M,
                                                                                                                                                                                                        (CHUS ) CHUGAI SEIYAKU KK
                                                                                                                                                                                                                                                                                                                                                  2002-682599/73
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hes 337; Conserv
                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; ABG97832
                                                                                                                                                                                                                                                                             Fukushima N,
                                                                                              17-APR-2001;
12-SEP-2001;
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ABK71405
ID ABK71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGCCCTGGACTCTGCTCCTCGTCACCCTCCTCAGGGCACAGGATCCTGGGCTCAG
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                                                          The present sequence is that of patient-specific bicistronic chimeric idlotype VR1642 (plasmid VAXID), which is used to treat B-cell lymphoma patients. The plasmid includes the cytomegalovirus immediate-early promoter, enhancer and 5' untranslated sequences, driving the expression of mouse-human chimeric immunoglobulin light and heavy chain sequences. The human light and heavy chain sequences. The bound cell lymphom cell line RAMOS. The transcriptional terminator region includes polyA and termination signals from the bovine growth hormone gene. According to the invention, co-administration of VR1642 with a plasmid (see AAF30314) encoding human Fms-like tyrosine kinase (Flt-3 ligand) provides a means of treating a patient with B-cell lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 7528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7528 BP; 1896 A; 1980 C; 1847 G; 1805 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse DNA encoding 12E10L light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 78.8%; Score 307.2; DB 2
Best Local Similarity 88.3%; Pred. No. 1.2e-83;
Matches 346; Conservative 0; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCGGAAGAGGACCCGGTTGACCGTCCTAGG 389
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Example 2; Page 101-106; 149pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-OCT-2001; 2001WO-JP09260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes a modified antibody comprising at least 2 heavy chain variable domains and 2 or more light chain variable domains of an antibody, and exhibits thrombopoietin (FPO) agonistic effect by causing the TPO receptor to crosslink. The antibodies are useful in preventives and/or remedies for platelet reduction-associated blood diseases, thrombocytopenia following cancer chemotherapy or leukaemia. The antibody can act as a TPO signal transduction agonist by transducing a signal into cells by crosslinking a TPO receptor to exert TPO agonism. This sequence encodes a thrombopoietin (TPO) agonist antibody associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                 Modified antibody, thrombopoietin, TPO; agonist,
TPO receptor, platelet reduction-associated blood disease,
thrombocytopenia, cancer chemotherapy, leukaemia, signal transduction,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Degraded thrombopoietin agonist antibodies containing H and L chain V domains of monoclonal antibody, useful in preventives and/or remedies for blood diseases, thrombocytopenia following cancer chemotherapy or
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                                                                                   DNA encoding thrombopoietin agonist antibody associated protein #25
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Yabuta N,
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17-APR-2001; 2001WO-JP03288.
12-SEP-2001; 2001JP-0277314.
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                                               (first entry)
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Matches 337; Conserva
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P-PSDB; ABG35333.
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The invention relates to isolated polynucleotide (1) and polypeptide (11) sequences. (1) is useful as hybridisation probes, polypeptide (11) sequences. (1) is useful as hybridisation probes, and sequence to polynucleotides are also used in diagnostics as expressed sequence tags for for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (11) or to treat disease states involving (11). (11) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (11) and its binding partners are useful in medical inaging of sites expressing (11). (1) and (11) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forenaics, gene mapping, identification of mutations in responsible for genetic disorders or other traits to assess broadersity
241 AATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 300
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                                                                         301 GCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding novel human diagnostic protein #19281.
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                                                                                                                                                                                                                           387
                                                                                                                                                                                                                                                                                             361 GGCGGAGGGACCAAGCTGACCGTCCTA 387
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                                                                                                                                                                                                                           361 GGAAGAGGACCCGGTTGACCGTCCTA
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23-AUG-2000; 2000US-0649167.
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Sequence 756 BP; 161 A; 240 C; 197 G; 158 T; 0 other;

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 Length 756;
 Score 306.8; DB 23; Length
Pred. No. 6.9e-84;
0; Mismatches 52; Indels
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                                                                                                                                                                                                                                    GGAAGAGGACCCGGTTGACCGTCCTAGGT 390
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  78.7%;
86.7%;
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2000US-0649167.
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Query Match
Best Local Similarity 86.7
Matches 338; Conservative
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P-PSDB; ABG22850.
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polymerase contain reaction (FLK) primers, originaries, constraint production of (II). The polymerase can also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymuclectide sequences have applications in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cannon acid sequences. AASéA197-AAS94564 represent novel human call sequences date for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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primers, oligomers, and for chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGGCCTGGACTCTGCTCCTCGTCACTCACTCAGGGCACAGGATCCTGGGCTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 23; Length 866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 866 BP; 200 A; 274 C; 213 G; 179 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 78.7%; Score 306.8; DB 2 Best Local Similarity 86.7%; Pred. No. 7.2e-84; Matches 338; Conservative 0; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human prostate expression marker cDNA 22576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eccesacidadecardadecercercerada 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABV22585 standard; cDNA; 1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200160860-A2
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TCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCTTGGACAGTCGATCACCCATCTCC 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCACTGGAACCAGCAGTGACATTGGGGGTTATAACCTATGTCTCCTGGTATCAACAACA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGTGGGCTCCA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGGTCCA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the precification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;

(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

(e) selecting a composition for inhibiting prostate cancer in a patient;

(f) assessing the prostate call carcinogenic potential of a compound;

(g) determining whether prostate cancer has metastasized in a patient;

(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGGCCTGGACTCTGCTCCTCGTCACCCTCCTCAGGGCACAGGATCCTGGGCTCAG 60
                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         patient;(I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 23; Length 1636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.3%; Score 305.4; DB 23; Length 89.2%; Pred. No. 2.5e-83; ive 0; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1636 BP; 345 A; 470 C; 479 G; 342 T; 0 other;
                                                                                                                                                                                                      (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 3949; 11750pp; English
                                                                                                                                                                                                                                            Schlegel R, Endege WO, Monahan JE;
                                                                            16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
                   20-FEB-2001; 2001WO-US05171
                                                                                                                                        18-JUL-2000; 2000US-219007P
13-DEC-2000; 2000US-255281P
                                                           2000US-183319P
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Best Local Similarity 89.2
Matches 354; Conservative
                                                                                                                                                                                                                                                                                     WPI; 2001-662795/76
                                                         17-FEB-2000;
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Search completed: December 29, 2003, 16:25:33 Job time : 172.16 secs

GGCTGAGGACGAGGCTGATTATTACTGCAGCTCATATACAAGCAGCAGCAGCACCACTCTATT 419

GGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACT-----TT 353

360 354 420

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucl	nucleic search, using sw model
Run on:	December 29, 2003, 16:08:50 ; Search time 1752.27 Seconds (without alignments) 9875.644 Million cell updates/sec
Title: Perfect score: 4 Sequence:	US-09-019-441-2 423 1 ATGAAACACCTGTGGTTCTTTCCTGGTCACCGTCTCCTCA 423
Scoring table: 1	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2888711 seqs, 20454813386 residues
Total number of P	hits satisfying chosen parameters: 5777422
Minimum DB seq le Maximum DB seq le	length: 0 length: 2000000000
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	GenEmbl:*  1: gb_ba:*  3: gb_htg:*  4: gb_om:*  4: gb_om:*  5: gb_pt:*  6: gb_pt:*  7: gb_pt:*  10: gb_rx:*  11: gb_yx:*  11: gb_yx:*  11: gb_yx:*  12: gb_yx:*  13: gb_ux:*  14: em_bx:*  15: em_bx:*  16: em_ox:*  17: em_ox:*  18: em_ox:*  19: em_ox:*  22: em_ox:*  23: em_bx:*  24: em_bx:*  25: em_ox:*  25: em_ox:*  26: em_ox:*  27: em_ox:*  28: em_ox:*  29: em_bx:*  29: em_bx:*  21: em_ox:*  22: em_ox:*  23: em_bx:*  24: em_bx:*  25: em_bx:*  25: em_ox:*  26: em_ox:*  27: em_bx:*  28: em_htg_ix:*  29: em_htg_ix:*  31: em_htg_ix:*  32: em_htg_ix:*  33: em_htg_ix:*  34: em_htg_ix:*  35: em_htg_ox:*  36: em_htg_ox:*  37: em_htg_ox:*  38: em_htg_ox:*  39: em_htg_ox:*  40: em_htg_ox:*  41: em_htg_ox:*  41: em_htg_ox:*  41: em_htg_ox:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query	Length	DB	OI.	Description
			435	σ	AF416358	6358 Papio
	32		441	σ	AF416359	16359 Papi
	323.8	76.5	420	σ (	MMU57560	US7560 Macaca mula
	75		4 4 C	ס מ	MMTE7563	Ses Macaca
			424	nσ	HSIGHXX28	10 H.sapi
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	3 6		453	σ	HSE5444	Z14196 H. sapiens r
	86		2149	, o	BC011857	BC011857 Homo sapi
	97		447	0	AF416357	AF416357 Papio cyn
	N		423	σ	HST14X24	Z75375 H.sapiens m
	296.6		429	σ	AF062232	AF062232 Homo sapi
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	94.		426	σ		F062278
	294.6	9.69	416	σ	HSIGHXX27	909 H.sapiens
	92.		1431	9	1088	8863 Sequenc
			;	•	70755107	o L u

## ALIGNMENTS

RESULT 1 AF416358	
rocns	AF416358 435 bp mRNA linear PRI 27-MAR-2002
DEFINITION	Papio cynocephalus anubis clone VH4-4 immunoglobulin heavy chain
	variable region mRNA, partial cds.
ACCESSION	AF416358
VERSION	AF416358.1 GI:19744277
KEYWORDS	
SOURCE	Papio anubis (olive baboon)
ORGANISM	Papio anubis
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
	Cercopithecinae, Papio.
REFERENCE	1 (bases 1 to 435)
AUTHORS	Scinicariello, F., Jayashankar, L. and Attanasio, R.

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                   SOURCE
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                                                                                                                                                                                                                                                                                                  /trānslation="MKHLWFPLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVS
GGSISSSXWSWTRQAPGKGLBWIGGIYSNSGWYYYNPSLKNRVTISTDTSKNQFSLKL
SSVTAADTAVYYCARDLGAYNWGPQHYWGQGVLVTVSSASASA"

131 c 131 c 124 g 12 t
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                   chains: identification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGGGAAGGGGCTGGAGTGGATTGGGGGTATCTATAGTAATAGTGGGAACACCTACTAC 237
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Baboon immunoglobulin variable region heavy chains: identification of genes homologous to members of the human IGHV1-IGHV7 subgroups 1mmunogenetics 53 (10-11), 815-820 (2002)
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G
                                                                                                                        Georgia
                                                                                                                                                                                                                                                                                                                                                                                9; Length 435;
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                                                                                Z (bases 1 to 435)
Scinicariello,F., Jayashankar,L. and Attanasio,R.
Direct Submission
Submitted (04-SEP-2001) Department of Biology, Ge
University, PO BOX 4010, Atlanta, GA 30302, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             Score 328.6; DB 9;
Pred. No. 1.7e-78;
0; Mismatches 49;
                                                                                                                                                                                                                                     1. .>435
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/db_xref="G1:19744278"
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mol_type="mRNA"

shb_species="anubis"

/db_xref="taxn:9555"

/clone="VH4-4"
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Best Local Similarity 87.7%;
Matches 371; Conservative
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                                                                                     Eukaryotta, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Papio.

1 (bases 1 to 441)
Scinicariello,F., Jayashankar,L. and Attanasio,R. Babon; immunoglobulin variable region heavy chains: identification of genes homologous to members of the human IGHVI-IGHV7 subgroupps immunogenetics 53 (10-11), 815-820 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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Pred. No. 4.7e-78;
0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (Dases 1 to 441)
Scinicariello,F., Jayashankar,L. and Attanasio,R.
Direct Submission
Submitted (OH-SEP-2001) Department of Biology, Ge
University, PO BOX 4010, Atlanta, GA 30302, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 .441
/organism="Papio anubis"
/mol_type="mRNA"
/sub species="anubis"
/db_xref="taxon:9555"
Papio anubis (olive baboon)
Papio anubis
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Best Local Similarity 86.9%;
Matches 373; Conservative
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SSVTAADTAVYYCARGDYSSNWWYFEFWGQGALVTVSS"
123 c 128 g 89 t
                                                                                                                                                                                                                                                                                           ימיוט /סלס (מרוים 11-FBB-1998 אמכסכם mRNA linear PRI 11-FBB-1998 Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC antibody, mRNA, partial cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A. Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A. and Capra, J.D.
Direct Submission
Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center, University of Texas Southwestern Medical Center, 6000 Harry Hines Blvd., Dallas, TX 75235-9140, USA
361 GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCC 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata, Vertebrata, Euteleostomi;
Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostor Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.

[ Loases 1 to 420]
Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Roubinet Blancher,A. and Capra,J.D.
Variable region gene segment utilization in rhesus monkey hybridomas producing human red blood cell-specific antibodies: predominance of the VH4 family but not VH4-21 (V4-34)
Mol. Immunol. 34 (3), 237-253 (1997)
                               CTGCAGCTGCAGGAGTCGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC
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| organism="Macaca mulatta"
| mol_type="mRNA"
| mol_type="mRNA"
| /mofe="hybridoma 1C9"
| . . >420
| codon_tatm=1
| /product="tarm=1
| /product="tarm=1
| /protein_id="AAC02642.1"
| /db_xref="d1:155078"
| /db_xref="d1:155078"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macaca mulatta (rhesus monkey)
Macaca mulatta
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AUTHORS
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GYSISSGYGWNWIRQPPGKGLEWIGSIGGSRGNTNHNPSLKSRVTISIDTSKNQFSLK
LRSLTAADTAVFYCARDGGYSSRFFDYWGQGVLVTVSS"
                                                                                                                                                                                                                                                                  Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.

Cercopithecinae; Macaca.

1 (bases 1 to 20)

Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Roubinet,F., Blancher,A. and Capra,J.D.
Variable region gene segment utilization in rhesus monkey bredominance of the VH4 family but not VH4-21 (V4-34)

MOLI Immunol. 34 (3), 237-253 (1997)
                                     PRI 11-FEB-1998
         MMUS7560 , 420 bp mRNA linear PRI 11-FEB-1991
Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC
antibody, mRNA, partial cds.
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Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.
and Capra, J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
University of TRAS Southwestern Medical Center, 6000 Harry Hines
Blvd., Dallas, TX 7525-9140, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Argadacaccieres de recretecres de recretecres de constantes de constan
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| codon start=1
| product="immunoglobulin heavy chain"
| protein id="AACO2637.1"
| db_xref="GI:1575068"
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Pred. No. 3.5e-77;
0; Mismatches 52
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/organism="Macaca mulatta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9544"
/note="hybridoma 1C8"
                                                                                                                                                                                                          Macaca mulatta (rhesus monkey)
Macaca mulatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 g
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HSIGHXX28 423 bp mRNA linear PRI 26-JUL-1997
H.sapiens mRNA for XLA IG heavy chain VDJ region (LE 4-8).
X65910 S58678
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                                                                                                                                                                                                                                                                                                     CTGAACCTGAACTCTGTGACCGCGGGGGGGCGGTGTATTACTGTGCCAGAGATTGG 360
                   61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
                                                                          TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC 180
                                                                                             CCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCCACCAACTAC 240
                                                                                                                                                                                                                                                                                                                          361 GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCC 420
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 423)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 heavy chain; immunoglobulin; joining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (08-APR-1992) C. Schiff, Centre D'Immunologie de Marseille, Case 906, 13288 Marseille, Cedes 9, FRANCE
2 (bases 1 to 423)
Milli, M. Le Deist, F., de Saint-Basile, G, Fischer, A.,
Fougereau, M. and Schiff, C.
Bone marrow cells in X-linke agammaglobulinemia express pre-B-specific genes (lambda-like and V pre-B) and present immunoglobulin V-D-J gene usage strongly biased to a fetal-like
                                                                                                                                                                                                                                                CTGCAGCTGCAGGAGTCGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC
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93232287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="LE 4-8"
/cell_type="pre-B"
/tissue_type="bone marrow"
/clone_lib="LE library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354. .377
/note="diversity region"
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∕organism≃"Homo sapiens"
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/note="joining region"
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/db_xref="taxon:9606"
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/note="variable
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diversity region; Ig
variable region.
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Homo sapiens
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HSIGHXX28
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AUTHORS
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/codon start=1

/product="immunoglobulin heavy chain"

/product="immunoglobulin heavy chain"

/product="immunoglobulin heavy chain"

/db_xref="c1:1575074"

/db_xref="c1:1575074"

/db_xref="c1:1575074"

/cranslation="MKHUMFPLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVS

GGSISSNYWWARNEQPERGERAIGREYGTSGSTYXNPSLTSRVTISTDTSKNQFSLKL

SSVTAADTAVYYCARYTVSKAFDYWGGGVLVTVSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cercopithecines, Macaca.

(bases 1 to 41)

Andris J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Roubinet, F., Blancher, A. and Captra, J.D.

Variable region gene segment utilization in rhesus monkey hybridomas producing human red blood cell-specific antibodies: predominance of the VH4 family but not VH4-21 (V4-34)

97368199
                                                                                                                                                                                                                                                                                                                                                                                 All bp mRNA linear PRI 11-FEB-1998 Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC antibody, mRNA, partial cds.
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                                         AACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC 300
                                                                CTGAACCTGAACTCTGTGACCGCCGCGCGCACACGCCGTGTATTACTGTGCCAGAGATTGG 360
                                                                                                                                        GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCCAGGGAGTCCTGGTCACCGTCTCC 420
                                                                                                                                                                                                                 CCAGGGAAGGGGCTGGAGTGGGAGTATCTATGGTAGTAGTGGGAGCACCACCGAATAC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 411)
Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A. and Capra, J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
Submitted (106-MAY-1996) J.S. Andris, Molecular Immunology Center,
University of Texas Southwestern Medical Center, 6000 Harry Hines
Blvd., Dallas, TX 75235-9140, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. 411
/organism="Macaca mulatta"
/mol_type="mRNA"
/db_xref="taxon:9544"
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Best Local Similarity 88.2%;
Matches 373; Conservative
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BASE COUNT ORIGIN

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1. .. s414
/codon start=1
/product==immunoglobulin heavy chain"
/product==immunoglobulin heavy chain"
/protocin id="AACO2645.1"
/db_xref="G1:1575084"
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GYSISSNYWSWIRQPPGKGLEWIGYIYGSSGSAYYNPSLKSRVTISIDTSKNQFSLKL
SSVTAADTAVYYKENPYGPTFPDYWQGVLVTVSS"
a 128 c 110 g 93 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anderson, D.R., Brams, P., Hanna, N., Shestowsky, W.S. and Heard Human B7.1-specific primatized antibodies and transfectomas expressing said antibodies expressing said antibodies Patent: US 6113898-A 11 05-SEP-2000; Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1431;
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                                                                                                                                                                                                             Score 314.6; DB 9;
Pred. No. 1.1e-74;
0; Mismatches 44;
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from patent US 6113898.
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462 c 385 g
            /note="hybridoma"
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84.5%;
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Best Local Similarity 87.5%;
Matches 370; Conservative
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1 (Dases I to 414)
Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Roubinet,F.,
Blancher,A. and Capra,J.D.
Variable region gene segment utilization in rhesus monkey
hybridomas producing human red blood cell-specific antibodies:
Most family but not VH4-21 (V4-34)
Mol. Immunol. 34 (3), 237-253 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MMU57568 414 bp mRNA linear PRI 11-FEB-1998
Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC
antibody, mRNA, partial cds.
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                                                                                                                                                                                 CTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
                                                                                                                                                                                                                                                                                                                       CCAGGGAAGGGACTGGAGTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAACTAC 240
                                                                                                                                                                                                                                                                                                                                          CTGAACCTGAACTCTGTGACCGCCGCGGACACGCCCGTGTATTACTGTGCCAGAGATTGG 360
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Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Blancher,A.
and Capra,J.D.
Direct Submission
                                                                                                                                                Macaca mulatta (rhesus monkey)
Macaca mulatta
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center, University of Fexas Southwestern Medical Center, 6000 Harry Hines Blvd., Dallas, TX 75:55-9140, USA Location/Qualifiers
                                                                                                                1 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
                                                                                  Gaps
                                                                                9
                                                 423;
                                                 Length
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                                             ore 315.6; DB 9;
ed. No. 5.9e-75;
Mismatches 49;
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/organism="Macaca mulatta"
/mol_type="mRNA"
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                                                 Score
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                                             74.6%;
ilarity 87.1%;
Conservative
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 84
                                             Query Match
Best Local Simi
Matches 371;
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

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LOCUS

RESULT 7 MMU57568 Bource

FEATURES

JOURNAL MEDLINE PUBMED

REFERENCE AUTHORS

TITLE JOURNAL

PAT 14-FEB-2001

and Heard, C.

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Howaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Butkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 1431)

RS Anderson, D.R.; Hanna, N., Brams, P. and Hard, C.
Identification of unique binding interactions between certain antibodies and the human B7.1 and B7.2 co-stimulatory antigens antibodies and the human B7.1 and B7.2 co-stimulatory antigens antibodies and the human B7.1 and B7.2 co-stimulatory antigens antibodies and the human B7.1 and B7.2 co-stimulatory antigens by Dactent: JP 2001504693-A/6

PP 10-APR-2001

PF 29-OCT-1997 UP 1998521633

PR 08-NOV-1996 US 08/746361

PI DARRELL RANDERSON, NABIL HANNA, PETER BRAMS, CHERYL HARD PC AALX39/395, CO7X16/18 (CO7X16/18 (CO7X16 (CO7X16 (CO7X16 (CO7X16 (CO7X16 (CO7X16 (CO7X16 (CO7X16 (CO7X16 
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                                                                                                               CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGATTGG 360
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181 CCAGGGAAGGGGCTGGAGTGGGAGTTTCTATAGTAGTAGTGGGAACACCTACTAC 240
                                                                  AACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACGCGTCCAAGAACCAGTTCTCC 300
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/mol_type="genomic DNA"
/db_tref="taxon:9606"
a 463 c 384 g 265
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JP 2001504693-A/6.
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Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 420)
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Submission
Submitted (08-APR-1992) C. Schiff, Centre D'Immunologie de
Submitted (08-APR-1992) C. Schiff, Centre D'Immunologie de
Marseille, Case 906, 13288 Marseille, Cedes 9, FRANCE
2 (bases 1 to 420)
Milli,M., Le Deist,F., de Saint-Basile,G., Fischer,A.,
Milli,M., Le Deist,F., de Saint-Basile,G., Fischer,A.,
Fougereau,M. and Schiff,C.
Bone marrow cells in X-linked agammaglobulinemia express
pre-B-specific genes (lambda-like and V pre-B) and present
immunoglobulin V-D-J gene usage strongly biased to a fetal-like
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                                                                                                    1 Angalacaccigregification concentration and a serious and
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/db xref="taxon:9606"
/chromosome="14"
/clone="15 4-5"
/cell type="pre="B"
/cisue type="bone marrow"
/clone_"1b="1E library"
  Mismatches
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Homo sapiens clone 21u-39 immunoglobulin heavy chain variable
region (IGH) mRNA, partial cds.
AP662100
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GGSISSSNWWSWVRQPPGKGLEWIGEIYHSGSTNYNPSLKSRVTISVDKSKNQFSLKL
SSVTAADTAVYYCARGPPDYGDYRFPDYWGQGTLVTVSSG"
                                                  CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGATTGG 360
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1 (bases 1 to 426)
1 (bases 1 to 426)
1 (mang,X. and Stollar,B.D.
1 Immunoglobulin VH gene expression in human aging Clin. Immunol. 93 (2), 132-142 (1999)
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Wang,X. and Stollar,B.D.
Direct Submission
Submitted (22-APR-1998) Biochemistry Department, Tufts University
School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
                                                                                                                                                                                                                                                           ------cgcTAGGCTTCTGGGGCCAGGGAGTC
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/protein_id="AAC18156.1"
/db_xref="G1:3170703"
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tissue_type="blood"
note="from elderly repertoire 21u"
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/organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/chromosome="14"
/map="4432.33"
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/gene="IGH"
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/cell_type="B lymphocytes"
/tissue_type="blood"
/dev_stage="adult"
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/note="G00-128-528"
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/note="G00-128-528"
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/gene="IGHV@"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCGCTGTCTCTGGTGGCTCCATCAGCAGTAGTAACTGGTGGACTTGGGTCCGCCAGCCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGGGAAGGGACTGGAGTTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGAACCTGAACTCTGTGACCGCCGCGGGACACGCCGTGTATTACTGTGCCAGAGATTGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGAAGCTGAGCTCTGTGACCGCCGCGACACGGCTGTGTATACTGTGCGACAGAGGTCG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ccagggaaggggagriggarirgggaaarcaarcaraggaag---caccaacrac 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACCCGTCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 determining region; immunoglobulin heavy
                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMIGHRH 420 bp mRNA linear PRI 09-NOV-1
Human (clone R5A3H) Ig rearranged H-chain mRNA V-region, 5' end
                                                                                                                                                                                                                                                                                                                                                                                             ATGAAACACCTGTGGTTCTTCCTCCTCGTGGCAGCTCCCCAGATGGGTCCTGTCTCAG
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                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                            3
                                                                                                                                                                                                                                                       Length 420;
                                                                                                                                                                                                                                               73.5%; Score 311; DB 9; Length 42
85.1%; Pred. No. 1e-73;
ive 0; Mismatches 60; Indels
                                                                                                                                                                         96
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/map="14932.33"
/sex="female"
           58. .352
/note="variable region"
353. .364
/note="diversity region"
                                                                                                               365. .420
/note="joining region"
123 c 127 g
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                                                                                                                                                                                                                                                     Query Match 73.5
Best Local Similarity 85.1
Matches 360; Conservative
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                                                                  misc_feature
                                                                                                                       misc_feature
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DEFINITION
ACCESSION
VERSION
KEYWORDS
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ORIGIN
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TITLE
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HUMIGHRH
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PUBMED
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120

9 9 180

COMMENT

SOURCE

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ST22X26 414 bp mRNA linear PRI 30-APR-1997 sapiens mRNA for Ig heavy chain variable region (VH4DJ) (clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tonnelle,C., D'Ercole,C., Depraetere,V., Metras,D., Boubli,L. and Fougereau,M.
Human thymic B cells largely overexpress the VH4 Ig gene family. A possible role in the control of tolerance in situ?
Int. Immunol. 9 (3), 407-414 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCTTGGAGACCTGTCCTCACC 120
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361 GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCC 420
                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                      ATGAAACACCTGTGGTTCTTCCTCCTCGTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 414)
Tonnelle, C.
Direct Submitted (26-UN-1996) Cecile Tonnelle, Centre d'Immunologie
Marseille Luminy, Marseille, 13288, France
Location/Qualifiers
                                                                                                                                                                                                                                                                      275399
275399.1 GI:2062062
275399.1 GI:2062062
immunoglobulin; immunoglobulin heavy chain; immunoglobulin
superfamily; variable region.
Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Mammalia; Lutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev stage="infant"
1. .414
/product="Ig heavy chain variable region (VH4DJ)"
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Pred. No. 3.1e-72;
0; Mismatches 49
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/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="maxA"
/chromosome="14"
/clone="T22.26"
/tissue type="b-lymphocyte"
/tissue type="thymus"
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Best Local Similarity 86.3%;
Matches 364; Conservative
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57. .351
/note="Ig \
352. .375
376. .414
                                                                             TCA 423
                                                                                                                   TCA 451
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                                                                                                                                                                                                                 LOCUS
DEFINITION
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                                                                                                                                                                            RESULT 15
HST22X26
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JOURNAL
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MEDLINE
                                                                                                                                                                                                                                                                          ACCESSION
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KEYWORDS
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                              셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gone- start=1
/product="immunoglobulin heavy chain VDJ region"
/protein_id="AAA20138.1"
/brotein_id="AAA20138.1"
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138 c 139 g t
                  468 bp mRNA linear PRI 27-JUL-1994
Human immunoglobulin heavy chain variable region (VH IV family)
From IgM rheumatoid factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 CCAGGGAAGGGCTGGAGTGGATTGGGGAATTCTATCATA---GTGGGAGCACCAACTAC 274
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                                                                                                                 L29122.1 GI:465144 | Tip heavy chain; rheumatoid factor; variable region subgroup VH-IV (aspiens (human) | Homo sapiens (human) | Homo sapiens
                                                                                                                                                                                               Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 468)

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Divaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Dasses 1 to 453)

1 (Dasses) 1 to 453)

2 NIH-MGC http://mgc.nci.nih.gov/

2 NIH-MGC http://mgc.nci.nih.gov/

2 Unpublished

2 Contact: Robert Strausberg, Ph.D.

2 Email: cgapbs-remail.nih.gov

3 Eco RI site shown at the beginning of the sequence.

7 Tisgue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LIAN at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward.
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UI-HF-BKO-aal-c-02-0-UI.r1 NIH MGC_36 Homo sapiens cDNA clone
IMAGE:3053955 5', mRNA sequence.
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COMMENT
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1 ATGAAACACCTGTGGTTCTT.....TCCTGGTCACCGTCTCCTCA 423
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Score

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ALIGNMENTS

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for average insert size l.8kb. Library constructed by Ling
Hong in the laboratory of Gerald Mn. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
RZPDLIB; I.M.A.G.E. CDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Reubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
pCMV-M13u, Primer sequence: CGTTGTAAAACGACGCCAGT.
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                                                                                                                            /tissue_type="germinal center B cells"
/cell_type="germinal center B cells"
/cell_type="germinal center B cells"
/lab_host="MHORGC36"
/lab_host="DH10B (LTI)"
/clone_lib="NHH MGC 36"
/note="Vector: pT7T3-Pac; Site 1: Not1; Site 2: Eco RI;
/constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Patima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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BX283435 NIH MGC 48 Homo sapiens cDNA clone IMAGp958G051281 ;
IMAGE:4565020, mRNA sequence.
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1 (bases 1 to 502)

Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.

Human UnigeneSet - RZPD3
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Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp958G051281.
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86.9%; Pred. No. 2...
... 0; Mismatches
                                                        organism="Homo sapiens"
                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3053955"
                cocation/Qualifiers
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="primary B-cells from tonsils (cell line)"
/lab host="primary B-cells from tonsils (cell line)"
/lab host="primary B-cells from tonsils (cell line)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells, Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXXhoI sites using the following 5' adaptor: GGGAGGGG, Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACCCGTCCATCAAGAGTCGAGTCACCATATCAGTAGACAAGTCCAAGAACCAGTTCTCC 319
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                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 862)
NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Hitp://mage.llnl.gov
Plate: LLCM1281 rows g column: 05

High quality sequence stop: 827.
  602438620F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565020 5'
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llarity 85.3%; Pred. No. 3.4e-66;
Conservative 0; Mismatches 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
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                                                                BG397580.1 GI:13291028
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                                                                                                       sapiens (human)
                       mRNA sequence.
                                                                                                                            Homo sapiens
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Site_2: BcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(6). Size-selected >50bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: Lib:s is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                             BG685428 101-MAC_48 Homo sapiens cDNA clone IMAGE:4764956 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               377 GGAGACATCTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACGTCTCC 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 867)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hog/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1623 row: a column: 21
High quality sequence stop: 637.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
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237 297 297

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/organism="Homo sapiens"
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/do_type="mRNA"
/do_type="mRNA"
/do_type="mRNA"
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AGENCOURT 6839001 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5761604
BQ072430
CTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 180
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1036)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
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Tissue procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI2810 row h column: 21
High quality sequence stop: 626.
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BRail: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOA1086CE07QPl&cluster=7198.r. Contact:
Feng Liang Email: fliang@lifetech.com URL
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOA1086CE07QPl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 890 bp mRNA linear EST 02-MAY-2003
CENTA COT 25-NORMALIZED Homo sapiens CDNA
                                                                                                                                          300
                                                                                                                                                                                                     320
                                                                                                                                                                                                                                                                                                        CTGAAGCTGAGCTCTGTGACCGCCGGGACACGGCCGTGTATTACTGTGCAGAGTCTGGG 380
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1 (bases 1 to 890)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
                                                                                                                                                                              CCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTAC
                                                           AACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC
                                                                                                                                                                                                                                                                       CTGAACCTGAACTCTGTGACCGCCGCGCCACGCCCGTGTATTACTGTGCCAGAGATTGG
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Pred. No. 3.6e-65;
0; Mismatches 46; Indels
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clone CS0D1086YJ13 5-PRIME, mRNA sequence.
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BX324929.1 GI:30338413
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Best Local Similarity 87.2%;
Matches 374; Conservative 0
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/organism="Homo sapiens"

/mol_type="mRNA"

/db xref="texon:9606"

/clone="IMAGE:6301263"

/clone="IMAGE:5301263"

/clone lib="NIH MGC ll3"

/clone lib="NIH MGC ll3"

/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:

ECORI; cDNA made by oligo-dT priming. Directionally cloned
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AGENCOURT_8485057 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301263
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11 (HagC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
                                                                                                                      423
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2516 row: n column: 16
High quality sequence stop: 560.
                                                                                                   5 AACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAGCTGC
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                                          Length 1036;
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                                                                       Indels
                                          297.4; DB 13;
No. 3.8e-65;
smatches 56;
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Tissue Procurement: Dr. Mark Watson
                                                                        Mismatches
197
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                                           Score
Pred.
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 283
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BQ710876
BQ710876.1 GI:21849775
                                          70.3%;
85.2%;
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Matches 357;
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921 bp mRNA linear EST 16-JUL-2002
AGENCOURT 8495271 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6302029
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into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
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Catarrhini; Hominidae; Homo.
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Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM518 row: n column: 14
High quality sequence start: 10
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                   DB 13; Length
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                                                                                                                                                                                                                                                                                                     62;
                                                                                                                                                                                                                                                Score 294.8; DB 1.
Pred. No. 1.7e-64;
0; Mismatches 62
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Primates;
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illarity 84.0%;
Conservative 0
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Mammalia; Eutheria;
1 (bases 1 to 921)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                         Ottenwaelder B., Obermaier B., Deutschenbaur S., Mewes H.W., Weil
Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
                                                                                                                                                                              German Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                              Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s wiemanndGdkZ-heidelberg.de; sequenced by MediGenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 532;
                                                                                                                                                                                                                                     al agguence also available.
This clone (DKPZp686M10219) is available at the RZPD in Ber
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
14059 Berlin-Charlottenburg, GBRMANY; Email: clone@rzpd.de
                                                                                                                    Submitted (07-MAY-2003) to the EMBL/GenBank/DDBJ databases MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 532 BP; 108 A; 163 C; 142 G; 114 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 293.8; DB 2;
Pred. No. 2.4e-64;
0; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="cDNA-collection"
                                                                                                                                                                  This is the 5' sequence of the clone insert
                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 69.5%;
Best Local Similarity 83.8%;
Matches 357; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCTCA 423
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                                                                                                      /lab host="DHIOS" (phage-resistant)"
/clone lib="NIH MGC 113"
/clone lib="NIH MGC 113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
ECRI; cDNA made by oligo-dT priming. Directionally cloned
into EcORI/XhoI sites using the following 5' adaptor:
GGCACGA(GG). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
"J13 c 244 g 176 t 2 others
                                                                                                                                                                                                                                                                                                                                 7
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                                                                                                                                                                                                                                                                                                                                                                                                                       AGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCTCACCTGCA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
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                                                                                                                                                                                                                                                                                                                                                                                            17 AACACCYGTGGTTCTTCCTCCTGCTGGCGGCTCCCAGATGGGTCCTGTCCCAGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens mRNA; EST DKFZp686M10219_r1 (from clone DKFZp686M10219)
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                    Length 921;
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                 90 ;
                                                                                                                                                                                                                                                                                                   Score 294; DB 13;
Pred. No. 2.7e-64;
0; Mismatches 60;
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Last updated, Version 1)
                                                  organism="Homo sapiens"
                                                                                             clone="IMAGE:6302029"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    뮵.
                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
       ity sequence stop: 6
Jocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expressed sequence tag
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       High quality
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Best Local S:
Matches 356
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HSM070357
                   FEATURES
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adjusted to have about out. The CDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2.000 - 3.000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5, primer and N(dT)14 as 3, primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded CDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted CDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli ToplOF' with
                                                                                                                                                                             KESTOUS) 467 bp mRNA linear EST 29-JAN-2003 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="Lyn80010281"
//clone lib="Organ: Liver; Vector: pCNS-D2; Site_1: EcoRI;
/note="Organ: Liver; Vector: pCNS-D2; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The CDNA vector was
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 467)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4470
Bmail: yongsung@mail.kribb.re.kr
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/db_xref="taxon:9606"
/clone="L7N80010281-6-D11"
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High quality sequence stop: 467.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo"
                                                                                                                                                                                                                                                                                                                                 CB138507.1 GI:28110281
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
Homo sapiens
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                            TCA 423
                                                                                 TCA 490
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ORIGIN
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                                                                                                                                                                                                                                                DEFINITION
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JOURNAL
                                                                                                                                                                  RESULT 11
CB138507
                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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                               EST 08-MAY-2003
                          BX377045
BX377045 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI001YJ13 5-PRIME, mRNA sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (basea I to 1201)
Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo saptens PLACENTA COT 25-NORMALIZED"
/note="list strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMYSPORT 6 vector. Library was normalized.
356 c 298 g 226 t 56 others
                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BMail: sequef@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198 r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI001CE07QPIscluster=7198 r. Contact :
ferg Liang Email: fliangelifetech.com URL :
http://fulllength.invitrogen.com/ luvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI001CE07QPI.
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/mol_type="mRNA"
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/clone="CS0DI001YJ13"
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/note="Organ: Liver; Vector: pCNS-D2; Site 1: ECORI;
Site_2" Noti; The pOly (A) * RAA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped intact mRNA was ligated with DNA-RNA linker including ECORI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with AT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The CDNA vector was adjusted to have about 60nt. The CDNA vector was adjusted to have about 60nt. The CDNA vector was circularized with E coli DNA ligase after digestion of ECORI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The converted to a DNA strand by Okayama-Berg method. The converted to a DNA strand by Okayama-Berg method. The converted to a DNA strand by Okayama-Berg method. The converted to a DNA strand by Okayama-Berg method. The converted cDNA library. After analyzing and sequencing about 2,000 - 3,000 colonies in original CDNA library, the abundant CDNA were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of products were used as template for synthesis of biotinylated single stranded CNNA propered from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli ToplOF' with electroporation method."
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0; Mismatches 62;
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Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
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K-EST0203106 L7NB0010281 Homo sapiens CDNA clone L7NB0010281-18-C09
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Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Vuseong-gu, Daejeon 305-333, South Korea
Tal: +82-42-860-4409
Fax: +82-42-860-4409
                                                                                                                                                                                                 62; Indels
                                                                                        DB 14;
                                                                                        Score 291.8; DB 1
Pred. No. 7.5e-64;
0; Mismatches 62
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/db_xref="taxon:9606"
/clone="L7N800102s1-18-C09"
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/organism="Homo sapiens"
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Plate: 18 row: C column: 09
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Location/Qualifiers
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/lab_host="Top10F'"
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CB147325
                                                                                  Query Match
Best Local Similarity 83.99
Matches 355; Conservative
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// Lab host="HDQ10F" "
// Clone lib="L5HLK1" "
// Site_2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (RAP) and then decapped with tabacco acid pyrophosphatase (RAP). The decapped intact mRNA was ligated with DNA-RNA linker including ECORI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The CDNA vector was adjusted to have about 60nt. The cDNA vector was circularized with E. Coll DNA ligase after digestion of ECORI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The
                                                                                                                                                                                                                                                                                                       Homo sapiens
Bukaryota, Metacoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
(bases 1 to 537)
(km,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF' by electroporation method. The CDNA libraries constructed by this method are full-length enriched cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Kim YS
Genome Research Center
Genome Research Institute of Bioscience & Biotechnology
Korea Research Institute of Dioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 27 row: F column: 01
High quality sequence stop: 537.
Location/Qualifiers
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K-EST0187880 L7N800102s1 Homo sapiens CDNA clone L7N800102s1-9-F04
5', mRNA sequence.
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241 AACCCGTCCACAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC 300
                                                                                                                                                                                                       301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGCCCGTGTATTACTGTGCCAGAGATTGG 360
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Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 9 row: F column: 04
High quality sequence stop: 552.
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/organism="Homo sapiens"
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products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli ToplOF' with electroporation method."
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K-2570205192 L7N80010281 Homo sapiens cDNA clone L7N80010281-21-A09
57, mRNA sequence.
CB148794
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Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Vuseong-gu, Daejeon 305-333, South Korea
Faz: +82-42-860-4470
Fax: +82-42-860-4409
                                                                                                                                                                                                                                   Score 291.8; DB 14; Length
Pred. No. 8e-64;
0; Mismatches 62; Indels
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                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L7N80010281-21-A09"
                                                                    organism="Homo sapiens"
Email: yongsung@mail.kribb.re.kr
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Location/Qualifiers
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421 TCA 423 |||| 453 TCA 455

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Copyright (c) 1993 - 2003 Compugen Ltd.
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(Updated on 25-MAR-2003 to correct PR field.)
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Matches 423; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Primatised anti-human B7.1 antigen antibody 16C10 heavy chain DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monoclonal antibody; cynomolgus monkey; macaque; 16C10; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenia purpura; systemic luque erythematosus; rheumatoid arthritis; psoriasis; type 1 diabbetes mellitus; graft versus host disease; hetero-hybridoma; transfectoma; ss.
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Matches 370; Conservative
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Chimeric Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= 16C10 heavy chain
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idiopathic thrombocycopaenia purpura, systemic lupus erythematosus, type in diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple sclerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours: Optionally the MAA can be conjugated to a drug or toxin. MAA so, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAA s are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 [11.2), T cell proliferation and antigen-specific immunoglobulin G (IgG) responses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of a primatised form of the heavy chain of 16C10 antibody
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Matches 370; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunogenicity;
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                                                                                                                                                                                                             --- CGCTAGGCTTCTGGGGCCAGGGAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complementarity determining region; antibody; primate; immunog Old World ape; Old World monkey; antigen-binding affinity; 86
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Pred. No. 2.7e-71;
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/product= "Heavy chain of 16C10 antibody"
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Cocation/Qualifiers
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Best Local Similarity 84.5%;
Matches 370; Conservative (
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                 TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC
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monoclonal antibody; chimaeric antibody; recombinant antibody; cynomolgus monkey; autoimmune disease; rheumatoid arthritis; cynomolgus monkey; autoimmune disease; rathematoid arthritis; leukaemia; lymphoma; graft-versus-host disease; asthma; transplant rejection; HIV; therapy; CE9 gamma-4B; ss.
show high affinity to human CD4, have little or no immunogenicity in humans and show reduced or absence of effector function. They can be used to treat autoimmune diseases such as rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 70.9%; Score 299.8; DB 18; Length 1404; Best Local Similarity 83.5%; Pred. No. 7.7e-68; Matches 353; Conservative 0; Mismatches 67; Indels 3;
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CD4; monoclonal antibody; chimaeric antibody; recombinant antibody; cynomolgus monkey; autoimmune disease; rheumatoid arthritis; leukaemia; lymphoma; graft-versus-host disease; asthma; transplant rejection; HIV; therapy; CE9 gamma-4PE; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gamma-4E and -4PE mutations confer activity enhanced stability and eliminate depleting activity. The antibodies can be used to treat autoimmune diseases such as rheumatoid arthritis.
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Pred. No. 7.7e-68;
0; Mismatches 67;
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                                                                                                                                                                                                                                                                                                                                                                                        Reff ME,
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Best Local Similarity 83.5%;
Matches 353; Conservative (
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                                                                        Chimeric antibody comprising monkey variable domains and human constant domains - affects CD4-mediated immune functions, esp. useful for treatment of autoimmune disease, e.g. rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 299.8; DB 1
Pred. No. 7.7e-68;
0; Mismatches 67
                                                                                                                                                                                       Disclosure, Page 86-88; 155pp; English
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Best Local Similarity 83.5%;
Matches 353; Conservative (
           WPI; 1997-201913/18
                                P-PSDB; AAW14926
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DB 18; Length 1404; Indels 240

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CCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAACTAC
                                        241 AACCCGTCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC
                                                                                                                                                                                                                                                                                                                                                               361 GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGGCCAGGGAGTCCTGGTCACCGTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 53-54; 92pp; English.
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92US-0856281.
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(first entry)
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08-JUN-1993
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                               358 ATATTGAAATATCTTCACTGGTTATTATACTGGGGCCAGGGAGTCCTGGTCACCGTCTCC 417
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GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCC 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention provides an antibody (Ab) comprising donor CDRs (complementarity determining regions) derived from a non-human antigenspecific donor antibody, and an acceptor framework from a non-human primate. The Abs are prepared by grafting CDRs from a non-human antigenspecific donor antibody onto homologous Old World ape or monkey acceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        frameworks. The Abs have reduced immunogenicity and are better tolerated in humans (because of the close similarity between the human and primate proteins), but retain the full antigen-binding affinity of the donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibodies containing donor complementarity determining regions and non-human primate acceptor frameworks, having reduced immunogenicity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complementarity determining region; antibody; primate; immunogenicity; old World ape; Old World monkey; antigen-binding affinity; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Argangcaccreterecricerecrecreses accreces are a secretered and a secretered accretered and a secretered accretered and a secretered accretered and a secretered accretered as a secretered and a secretered accretered as a secretered accretered accretered as a secretered accretered ac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of Cynomologous VH cDNA clone 2-10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Page 84-85; 123pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                   AAZ39335 standard; DNA; 420 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence
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Best Local {
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23-MAR-1992;
25-JAN-1995;
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                                                                                                                                                                                                                                                                                                                                                                  GCCCAAATAGCTGGAACAACGCTTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCC 420
                                                                                                                                             CIGCAGCIGCAGGAGICGGGCCCAGGAGIGGIGGAGCCTICGGAGACCCIGICCCTCACC 120
                                                                                                                                                           GTGCAGCTGCAGGAGGCGGGCCCAGGACTGAAGCCTTCGGAGACCCTGTCCTCACC 123
                                                                                                                                                                                       TGCGCTGTCTCTGTGTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC 180
                                                                                                                                                                                                             124 TGCAGTGTCTCTGGTGGCTCCATCAGCGGTGACTATTATTGGTTCTGGATCCGCCAGTCC 183
                                                                                                                                                                                                                                                      CCAGGGAAGGGACTGGAGTGGATCGGCTACATCTATGGCAGTGGTGGGGGCACCCAATTAC 243
                                                                                                                                                                                                                                                                                                  AATCCCTCCTCAACAATCGAGTCTCCATTTCAATAGACACGTCCAAGAACCTCTTCTCC 303
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                                                                                                 1 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
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                                                                              Gaps
                                                                            ä,
                                                       DB 14; Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-CD4 antibody; cynomolgus monkey; immunoglobulin; Ig. chimpanzee; chimeric antibody; human therapy; Old World
                                                                            68; Indels
                                  Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;
                                                     Score 298.2; DB 1-
Pred. No. 1.5e-67;
0; Mismatches 68
 immunological disorders. (Updated on 25-MAR-2003 to correct PN field.)
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/*tag= a
/product= Anti-CD4 VH_region
/note= "No stop codon given"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT91564 standard; DNA; 423 BP
                                                     Query Match 70.5%;
Best Local Similarity 83.2%;
Matches 352; Conservative
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91US-0735064
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25-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-1995;
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16-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A new chimeric antibody (Ab) has been developed comprising a human or chimpanzee immunoglobulin (Ig) constant region and an Old World monkey antigen (Ag)-binding region. The present sequence encodes an anti-CD4 cynomolgus monkey Ig heavy chain variable region. An anti-CD4 antibody (Ab) comprising the light- and heavy-chain variable regions encoded by the present sequence and that of AAT91565 is also new. The Abs are useful for human therapy, especially of tumours. Old world monkeys are sufficiently different from humans to allow Abs against human Ags, even relatively conserved Ags such as CD4 and CD54, to be raised in these monkeys, and are sufficiently similar to humans to avoid host anti-Ab immune responses when the Abs are introduced into humans. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 33; Fig 13; 46pp; English.
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                                                                                                                                                                                               Raab RW;
92US-0856281
95US-0379072
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Best Local Similarity 83.2
Matches 352; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antigen-binding region
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                                                                                                                                                                                                                                                                                  WPI; 1997-424183/39
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CTGAACCTGAACTCTGTGACCGCCGCGCACACGCCGTGTATTACTGTGCCAGAGATTGG 360
               Nucleic acid encoding hybrid antibody antigen-binding region and human or cl
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4..420
/*tag= a
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                                                                                                                                                                                         BP.
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92US-0856281.
95US-0379072.
95US-0481869.
                                                                                                                                                                                          DNA; 423
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                                                                                                                                                                                          standard;
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07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This DNA encodes the heavy chain variable region (VH) of the cynomolgus monkey anti-CD4 antibody. The antibody comprises antigan-binding sequences from an Old World monkey antibody and human constant domain sequences. The antibody specifically binds to CD4 and can be used in the treatment of rheumatoid or psoriatic arthritis.
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                                                  Anti-CD4 antibody; antigen-binding; treatment; chimeric; human; monkey; rheumatoid arthritis; psoriatic arthritis; ss.
                                                                                                                                                                 /transl_except= (pos:415..417, aa:Ser)
/product= "Variable heavy chain antigen binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treatment of rheumatoid and psoriatic arthritis - comprises administration of chimeric human-monkey anti-CD4 antibody
                         Anti-CD4 antibody variable heavy (VH) region encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68; Indels
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Pred. No. 1.5e-67;
0; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim -2; Columns 35-36; 47pp; English
                                                                                                                            Location/Qualifiers
                                                                                                                                                                                           region"
                                                                                                                                                                                                                                                                                                                                                                                                  Raab RW;
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                                                                                       Chimeric - Macaca cynomolgus.
Chimeric - Homo sapiens.
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91US-0735064.
92US-0856281.
92US-0912292.
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Matches 352; Conservative
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10-JUL-1992
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n: chimpanzee; hybrid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the coding sequence for the heavy chain variable region from an anti-human CD4 immunoglobulin raised in cynomolgus monkeys. The sequence was PCR amplified and used in the construction of a recombinant antibody comprising: (i) an Old World monkey Ig antigen-binding region; and (ii) a human or chimpanzee Ig constant region. The hybrid antibodies can be used as passive or active therapeutic agents against human diseases, e.g. B-cell lymphoma, AIDS, autoimmune and inflammatory diseases, transplant rejection or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "Ig heavy chain variable region"
/note= "no stop codon given at the 3' end of sequence"
                                                                                                                            361 GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer; PCR; amplification; leader sequence; human; monkey; baboon; macaque; immunoglobulin; heavy chain variable region; chimpanzee; hyb: lymphoma; AIDS; autoimmune disease; inflammatory disease; transplant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monkey anti-CD4 heavy chain variable region coding sequence.
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chimp constant region
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95US-0476237. 98US-0082472. 91US-0735064. 92US-0856281. 95US-0397072.

Raab

Hanna N,

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2003-182483/18

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(IDEC-) IDEC PHARM CORP
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23-MAR-1992;
                                                               17-APR-1995;
              37-JUN-1995
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tumours, or for producing therapeutic and diagnostic conjugates. Although evolutionary distant monkeys are used to raise antibodies against human antigens, they are sufficiently similar that they produce antibodies similar to human antibodies, such that when the monkey antibodies are introduced into humans, no host anti-antibody response
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
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                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunoglobulin constant region; immunoglobulin variable region; autoimmune response; rheumatoid arthritis; eczema; lymphoma; immunomodulatory disease; leukaemia; Hashimoto's thyroiditis; autoimmune carditis; Addison's disease; type I-diabetes mellitus; multiple sclerosis; male infertility; autoimmune hemolytic anaemia; inflammatory bowel disease; Sjogren's syndrome; psoriasis;
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                                                                                                                    DB 19; Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding cynomolgus monkey immunoglobulin heavy chain.
                                                                                                                                             Indels
                                                                                          Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;
                                                                                                                                             68;
                                                                                                                  70.5%; Score 298.2; DB 1
llarity 83.2%; Pred. No. 1.5e-67;
Conservative 0; Mismatches 68
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                                                                                                                                 Similarity
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                                                                                                                                   Best Local Simi
Matches 352;
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                                                                                                                     Query Match
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                                                                                                                                 Local
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The invention describes a recombinant antibody comprising a human, chimpanzee or a first old world monkey immunoglobulin constant region, and an antigen-binding portion of a second old world monkey immunoglobulin variable region. The first and second old world monkey immunoglobulin variable region. The first and second old world monkey can be the same or different. The recombinant antibody is useful for treating a tumour antigen, or for treating a tumour antigen, or for treating a buman having a tumour antigen, or for treating a nucliammune response (where the antigen is involved in a suffering from an autoimmune response (where the antigen is involved in an autoimmune response in the human). In particular, the recombinant antibody is useful for treating rheumatoid arthritis, eczema, or an immunomodulatory disease. The recombinant antibody is also useful for treating tumours, leukaemia, lymphoma, Hashimoto's thyroiditis, autoimmune carditis, Addison's disease, type Idiabetes mellitus, multiple sclerosis, male infertility, autoimmune hemolytic anaemia, inflammatory bowel disease, Sjogrem's syndrome, psoriasis, or systemic lupus erythematosus. This is the amino acid sequence of a monkey immunoglobulin heavy variable chain polypeptide for creation of the
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New recombinant chimeric antibodies comprising human, chimpanzee and Old World monkey portions, useful for treating e.g. cancer, eczema, leukemia, lymphoma, Hashimoto's thyroiditis, multiple sclerosis or male
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Pred. No. 1.5e-67;
0; Mismatches 68; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;
                                                                                                                                                                  Disclosure; Page 19-20; 101pp; English
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Best Local Similarity 83.2
Matches 352; Conservative
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systemic lupus erythematosus

Macaca cynomolgus

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08-MAY-2001; 2001US-0850165

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an antibody to human CD40, or its functional fragment, has at least one of the following properties: acting on dendritic cells to produce IL-12 in the presence of LP8 (lipopolysaccharide) and IFNgamma (interferon gamma); acting on dendritic cells to activate maturity of the dendritic cells with high G28-5 antibody; and activating CD95 expression with high G28-5 antibody against B cell line. Such antibodies or functional fragments can be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunoactivators, anti-tumour agents, immunosuppressants, and as remedies for autoimmune diseases, allergy or coagulation factor VIII inhibitors syndrome. This polynucleotide sequence represents a coding DNA sequence relating to the anti-CD40 monoclonal antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                   Antiallergic; haemostatic; immunomodulator; cytostatic; antibody; human CD40; IL-12; LPS; lipopolysaccharide; IFNgamma; interferon gamma; dendritic cell; high G28-5; B cell line; immunoactivator; anti-tumour agent; immunosuppressant; allergy; autoimmune disease; coagulation factor VIII inhibitor; anti-CD40; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-CD40 monoclonal antibody with antagonist/agonist activity to CD4( or functional fragment, is useful in the treatment of e.g. autoimmune
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                                                                                                                                                                                                                                                                                                                     Anti-CD40 monoclonal antibody related DNA SEQ ID No 43.
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84.6%; Pred. No. 4.1e-67;
ive 0; Mismatches 59
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                                                                                                                                                                        ABT31871 standard; DNA; 481 BP.
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11-MAY-2001; 2001UP-0142482.
05-OCT-2001; 2001US-0040245.
26-OCT-2001; 2001US-0040245.
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                                                                                                                                                                                                                                                                          (first entry)
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59; Indels

358; Conservative

Matches

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1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG

CTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAGGCCTTCGGAGACCCTGTCCCTCACC 120 52 ATGAAACATCTGTGGTTCTTCCTTCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 111

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240
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112 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 171
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Job time : 185.558 secs
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Sequence 198, App Sequence 198, App Sequence 7, Appli Sequence 963, App Sequence 1, Appli Sequence 7, Appli Sequence 1, Appli

Sequence 2, Appli Sequence 110, App Sequence 106, App

Sequence 114, Ap Sequence 74, Appl Sequence 16699,

Sequence 9,

Appli Appli

Sequence 3 Sequence 3 Sequence 3

Sequence 13, Appl Sequence 21201, A Sequence 1375, Ap Sequence 16650, A

Sequence 210, App Sequence 4, Appli

Sequence 4, Sequence 43, Sequence 4,

4, Appli 1, Appli 13582, A 114467,

Sequence Sequence

Sequence 114467, Sequence 114467,

Run on:

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Sequence 2, Application US/09019441
Publication No. US20030086921A1
GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
KLOFIZER, William S.
NAKAMURA, Takehiko
TITLE OF INVENTION: AMTIBODIES AND USE THEREOF AS THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDED ADDRESS:
CORRESPONDED ADDRESSE:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
COUNTRY: United States
TIP: 22131-3140
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,441
FILING DATE: 05-Feb-1998
CLASSIFICATION: CURROWN>
0 US-09-948-429B-3
3 US-10-124-807-3
3 US-10-291-532-3
4 US-10-291-532-3
4 US-10-124-905-3
4 US-10-309-774-106
3 US-10-309-774-106
3 US-10-309-774-106
3 US-10-309-774-114
1 US-09-918-995-16699
1 US-09-918-995-16699
1 US-09-925-299-198
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US-10-198-846-13582
US-10-027-632-114467
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APPLICATION NUMBER: US 08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INPORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 55,030
REFERENCE/DOCKET NUMBER: 012712-502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                            413
393
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                                                                                                                                                                                                                                        ; Search time 611.125 Seconds
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1 ATGAAACACCTGTGGTTCTT......TCCTGGTCACCGTCTCCTCA
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_MEW_PUB.seq:*
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                                         GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-10-103-686-2
US-10-124-807-11
US-10-124-807-11
US-10-291-512-11
US-10-291-512-11
US-09-905-243-40
5 US-10-211-357-9
5 US-10-211-357-9
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2313.2
2313.2
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20013.2
2009.8
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                                                                                                                                                                         OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
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Database

TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-6620

Appli , Appl Appl

US-09-850-165-15 US-10-211-357-1 US-10-300-675-1

Result Š. 836-2021

TELEFAX: (703) 836-INFORMATION FOR SEQ ID NO: 2:

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61 crecaecrecaeaerceeecccaeaereereaaeccrrceeaeaccrercerercae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGATTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                         Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 423; DB 15;
ilarity 100.0%; Pred. No. 2.3e-116;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                          NAME: TERKIN, ROBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE, DOCKET NUMBER: 012712-353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
                                                                              APPLICATION NUMBER: US/10/103,686
FILING DATE: 25-Mar-2002
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
                         SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>ر</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: mat_peptide;
; LOCATION: 58..423
; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-103-686-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 11, Application US/09948429B ; Patent No. US20020177689A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1..423
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US-09-948-429B-11
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ccaegeaaegeactegaetregaceratcrereragregregeeceaccaacrac 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACCCGTCCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 423; DB 11;
; Pred. No. 2.3e-116;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                     LOCATION: 58.7423
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10103686
Publication No. US20030059424A1
GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
NAKAMURA, Takehiko
                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                          mat_peptide
58..423
                         LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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CITY: Alexandria
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                              1..423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     423; Conservative
                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
US-10-103-686-2
                                                                                                                                                                                                                                                                                                                                                                                              US-09-019-441-2
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Best Local
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Gaps

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180 180 300 300

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GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACCUPITAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: 699 Prince Street
                                                                                    405
301 CTGAACCTGAACTCTGTGACCGCGCGCGCACACGGCCGTGTATTACTGTGCCAGAGATTGG 360
                                        361 CTTTTTCAGTTGTTGGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCGGGAGTC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTCTCTCCCAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13; Length 1431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 74.0%; Score 313.2; DB 1 Best Local Similarity 84.5%; Pred. No. 1.6e-83; Matches 370; Conservative 0; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PREDICATION NUMBER: 09/383,916
FILING DATE: 07-UNH-1995
ATTORNEY/AGENT INFORWATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/10124807
Publication No. US20030166207A1
                                                                                         361 GCCCAAATAGCTGGAACAA----
                                                                                                                                                                                                   TYPE: nucleic acid_
STRANDEDNESS: not relevant
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                 406 CTGGTCACCGTCTCCTCA
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LOCATION:
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; LOCATION:
US-10-124-807-11
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       "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
12
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Pred. No. 1.6e-83;
0; Mismatches 53; 1
                                                                                                                                                                                                                                                                 ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
FILING DATE:
                  TITLE OF INVENTION: "MONESY MONOCLONAL ANTIBOD TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS TITLE OF INVENTION: IMMUNOSUPPRESANTS" NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: ADDRESSE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-UTN-1995
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, ROBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         012712-131
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PRIOR APPLICATION DATA:
PLICATION NUMBER: 09/383,916
FILING DATE:
    Darrell R.
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TYPE: nucleic acid
STRANDEDNESS: not relevant
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Best Local Similarity 84.5%;
Matches 370; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: peptide
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FEATURE:
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; LOCATION:
US-09-948-429B-11
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                                                                                                                                                                                                                                                   COUNTRY:
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US-10-291-532-11

Sequence 11, Application US/10291532

Publication No. US20030180290A1

GENERAL INFORMATION:

APPLICANT: HARIHARAN, KANDASAMY

APPLICANT: HARIHARAN, NABIL

TITLE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC

TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES

FILE REFERENCE: 307003/291872

FILE REFERENCE: 2002-11-12

PRIOR FILING DATE: 2002-11-12

PRIOR FILING DATE: 2001-01-2

PRIOR PLICATION NUMBER: 09/758,173

PRIOR FILING DATE: 1999-08-26

PRIOR PRIOR DATE: 1999-08-26

PRIOR PLING DATE: 1999-08-36

PRIOR PLING DATE: 1999-08-36
                                                                                                                                                                                                                                                                                                                                                                    CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGATTGG 360
                                                                                           GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCCACC 120
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                                                                    CTGCAGCTGCAGGAGTCGGGCCCAGGAGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: primatized nucleotide sequence
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74.0%; Score 313.2; DB 13; Length
Best Local Similarity 84.5%; Pred. No. 1.6e-83;
Matches 370; Conservative 0; Mismatches 53; Indels
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TYPE: DNA
ORGANISM: Artificial Sequence
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; LOCATION: (1)..(1428)
US-10-291-532-11
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1 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG

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GENERAL INFORMATION:

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GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street

GITTLE OF DATA ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

GITTLE OF SEQUENCES:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

GITTLE OF SECURITION:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

GITTLE OF SECURITION:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

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ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

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GITTLE OF SECURITION:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

GITTLE OF SECURITION:

GENERAL OF SECURIT
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1 ATGAAACACCTGTGGTTCTTCCTCCTCGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
                                                                                                                                                                               121 TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC
                                                                                                                   61 CTGCAGCTGCAGGAGTCGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 CCAGGGAAGGGACTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTAC
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,905
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: 08 08/487,550
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 012712-131
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEPHONE: 703-836-620
TELEPHONE: 703-836-2021
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: Monoclonal Antibodies with Reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.6e-83
                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 012712-256
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84.5%; Pred. No. 1.6e
iive 0; Mismatches
                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/746,361
FILING DATE: 08-NOV-1996
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
                          APPLICATION NUMBER: US/10/073,138
FILING DATE: 13-Feb-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1..1431
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                   NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 GCCCAAATAGCTGGAACAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 40, Application US/09905243; Patent No. US20020062009A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1431 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGTCACCGTCTCCTCA
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Matches 370; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTAC 240
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BRAMS, Peter
TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OFFATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                             DB 14;
                                                                                                                                                                                                                                                                                                                                                                                         Score 313.2; DB 14;
Pred. No. 1.6e-83;
0; Mismatches 53;
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Publication No. USZO020187146A1
GENERAL INFORMATION:
APPLICANT: ANDERSON, Darrell R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE,
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
STATE: Virginia
COUNTRY: United States
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Best Local Similarity 84.5%;
Matches 370; Conservative
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                    STRANDEDNESS: not re.
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
   nucleic acid
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                                                                                                                                                              CDS
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LOCATION:
US-10-124-905-11
                                                                                                                                                              NAME/KEY:
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Ardahakcaccrerestricriccrecrestrestrescaetececeaniesereristrestens 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 70.9%; Score 299.8; DB 15; Length 1404; Best Local Similarity 83.5%; Pred. No. 1.6e-79; Matches 353; Conservative 0; Mismatches 67; Indels 3;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/211,357
                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 012712-165 TELECOMMUNICATION INFORMATION:
                                                                                                                                              FILING DATE: 05-Aug-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/612,914A
                                                                                                                                                                                                                                             FILING DATE: 10-Jul-2000
APPLICATION NUMBER: US 08/523,894
FILING DATE: 06-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 7: US-10-211-357-7
                                                                                                                                                                                                                                                                                                                                         NAME: Teskin, Robin L. REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 7:
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LENGTH: 1404 base pairs
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MOLECULE TYPE: DNA (genomic)
POSITION IN GENOME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION:
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Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
Therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 423;
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CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
CUNTX: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                    71.2%; Score 301.2; DB 9;
85.0%; Pred. No. 5e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
  TITLE OF INVENTION: Immunogenicity
FILE REFERENCE: P50770
CURRENT APPLICATION NUMBER: US/09/905,243;
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/300,970
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 97
SEQ ID NO 40
LENGTH: 423
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                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Macaca cynomolgus
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Matches 362; Conservative
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; LOCATION: (1)
US-09-905-243-40
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US-10-211-357-7
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NAME: Teekin, Robin L.
REGISTRATION UNMBER: 35,030
REFERENCE/DOCKET NUMBER: 01.
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ADDRESSER: BURNS, DOANE, STREET: 699 Prince Street
CITY: Alexandria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 11, Application US/10211357; Publication No. US/2030077275A1
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
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MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                              Newman, Roland A.
Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
Therapy
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STATE: VA

COUNTYER READABLE FORM:
MEDIJUN TYBE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/211,357
FILING DATE: 05-Aug-2002
CLASSIFICATION DATA:
APPLICATION NUMBER: US/09/612,914A
FILING DATE: 06-SEP-1995
ATTORNEY AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
RETERPHONE: 703-836-6620
TELEPHONE: 703-836-620
TELEPHONE: 703-836-2021
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 59 CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNNS, DOANE, STREET: 699 Prince Street
                                                                                               Sequence 9, Application US/10211357
Publication No. US20030077275A1
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
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LOCATION:
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418 TCA 420
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Reff, Mitchell B.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human Therapy
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/211,357
FILING DATE: 05-Aug-2002
CLASSIFICATION: UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/612,914A
FILING DATE: 06-SEP-1995
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            Query Match
Best Local Similarity 83.23
Matches 352; Conservative
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358 ATATTGAAATATCTTCACTGGTTATTATACTGGGGCCAGGGAGTCCTGGTCACGTCTCC 417
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          POSITION IN GENOME:
CHROMOSOME/SEGMENT: heavy chain gamma 4 with the P and
mutation
                                                                                                                                                                                                                  DB 15; Length 1404;
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US-09-905-243-44
; Sequence 44, Application US/09905243
; Patent No. US-0020062009A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
; TITLE OF INVENTION: Immunogenicity
; FILE REFERENCE: P50770
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/300,970
; PRIOR PILING DATE: 1999-04-28
                                                                                                                                                                                                                Query Match 70.9%; Score 299.8; DB 1
Best Local Similarity 83.5%; Pred. No. 1.6e-79;
Matches 353; Conservative 0; Mismatches 67
                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 44
LENGTH: 420
ORGANISM: Homo sapiens
                                                                                                                                 mat_peptide
                                                                                                  1..1404
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ORGANISM: Macaca cynomolgus
FRATURE:
NAME/KEY: CDS
LOCATION: (1)...(420)
US-09-905-243-44
                                                              FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                               NAME/KEY:
LOCATION:
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APPLICANT: HANNA, NABIL
APPLICANT: HANNA, NABIL
TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
FILE REFERENCE: 037003-0280614
CURRENT APPLICATION NUMBER: US/09/850,165
CURRENT FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: 09/082,472
PRIOR APPLICATION NUMBER: 09/082,472
PRIOR PILING DATE: 1998-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-17
PRIOR FILING DATE: 1992-03-3
PRIOR PLING DATE: 1992-03-3
PRIOR PLING DATE: 1992-07-10
PRIOR PLING DATE: 1992-07-10
PRIOR PLING DATE: 1992-07-10
PRIOR PLING DATE: 1992-07-10
PRIOR PLING DATE: 1992-07-11
                    Length 420;
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                    DB 9;
Score 298.2; DB 5
Pred. No. 3.9e-79;
0; Mismatches 68
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Patent No. US20020150580A1
GENERAL INFORMATION:
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35,030
                                     REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Monkey
                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 420 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                               mat_peptide
                                                                                                    TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 1:
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Best Local Similarity 83.1%;
Matches 349; Conservative
                                                                                                                                                                                  TYPE: nucleic acid
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                                                                                                                                          1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT
                                                               Length
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                                                            DB 10;
                                                          Score 298.2; DB 1
Pred. No. 3.9e-79;
0; Mismatches 68
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APPLICATION NUMBER: US/09/612,914A
FILING DATE: 10-701_200
APPLICATION NUMBER: US 08/523,894
FILING DATE: 06-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/10/211,357
FILING DATE: 05-Aug-2002
CLASSIFICATION: <URLOWN>
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ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSER: BURNS, DOANE, STREET: 699 Prince Street
CITY: Alexandria
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Publication No. US20030077275A1
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
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Reff, Mitchell E.
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                                                          70.5%;
                                                                                                Matches 352; Conservative
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; LOCATION: (4)..(420)
US-09-850-165-15
                                                                               Similarity
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                                                        Query Match
Best Local
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Publication No. US20030198638A1
GENERAL INFORMATION:
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
FILE REFERENCE: P-IX 5519
CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US/10/300,675
CURRENT FILING DATE: 2002-11-19
PRIOR PLING DATE: 2001-11-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 295.2; DB 15;
Pred. No. 3.1e-78;
0; Mismatches 68;
: 012712-165
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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FastSEQ for Windows Version 4.0
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69.4%; Score 293.4; DB 13; Length 417;
Best Local Similarity 84.2%; Pred. No. 1.1e-77;
Matches 356; Conservative 0; Mismatches 61; Indels 6;
; SEQ ID NO 1
; LENGTH: 417
; TYPE: DNA
; OKGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(417)
US-10-300-675-1
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Search completed: December 30, 2003, 03:42:09 Job time: 613.125 secs

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Title: Perfect score:

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Scoring table:

Searched:

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PATENTE NO. 6011139

PAPLICANT: REFF, Mitchell E.
APPLICANT: REFF, Mitchell E.
APPLICANT: REFF, Mitchell E.
APPLICANT: RACETZER, William S.
APPLICANT: NAKAWURA, Takehiko
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
TITLE OF INVENTION: AMYIBODIES AND USE THEREOF AS THERAPEUTICS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STATE: Virginia
COUNTRY: United States
COMPUTRY: United States
STATE: Virginia
COMPUTRY: IBM PC compatible
COMPUTRY: IBM PC compatible
COMPUTRY: BE PC COMPATIBLE
COMPUTER: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CLASSIFICATION: APPLICATION AND APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FBB-1997
CLASSIFICATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELECOMMUNICATION FOR SEQ ID NO: 2:
SEQUENCE: A32 hase apicies
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                                                          US-08-468-671-5
US-08-545-809A-55
US-09-260-527-4
US-08-545-809A-61
US-08-545-809A-9
US-08-545-809A-9
US-08-450-578-9
US-08-450-578-9
US-09-017-628-9
                S-09-582-337-13
S-08-545-809A-28
S-08-259-372A-5
S-08-468-671-5
 US-08-758-417A-199
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US-08-545-809A-59
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FEATURE:
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TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION:
FEATURE:
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US-08-803-085-2
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257.4
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Sequence 15
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Sequence 3
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Sequence 1
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-523-894-9
US-08-523-894-9
US-08-79-072A-19
US-08-481-869-19
US-08-476-237-15
US-08-476-331-107
US-08-476-349A-107
US-08-523-894-1
US-08-672A-17
US-09-672A-17
US-09-672A-17
US-09-672A-17
US-08-758-417A-205
US-09-042-353-355
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Maximum Match 100%
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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Score

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; Sequence 11, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGGTCACCGTCTCCTCA 438
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SDNESS: not relevant
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Best Local Similarity 84.5%;
Matches 370; Conservative
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                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
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MEDIUM TYPE: Floppy
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ADDRESSEE: BURNS, DC
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NAME/KEY:
LOCATION:
US-08-487-550-11
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APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: IMMUNOSUPPRESANTS"

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300
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                                                                                           1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
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APPLICATION NUMBER: US/08/487,550 FILING DATE: 07-JUN-1995 CLASSIPICATION: 435
   100.0%; Pred. No. 6.7e-114; ive 0; Mismatches 0;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Teekin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 0127
TELECOMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEPHONE: 703-836-6201
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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                                  423; Conservative
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COMPUTER READABLE FORM
MEDIUM TYPE: Floppy
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US-08-487-550-11
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TITLE OF INVENTION: "MONNEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
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        DB 3;
Score 313.2; DB 3
Pred. No. 8.7e-82;
0; Mismatches 53
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MOLECULE TYPE: DNA (genomic)
POSITION IN GENOME:
Newman, Roland A.
Reff, Mitchell E.
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Best Local Similarity 83.5%;
Matches 353; Conservative
                                                                                                                  ADDRESSEE: BURNS, DOANE,
STREET: 699 Prince Street
CITY: Alexandria
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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CHROMOSOME/SEGMENT:
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ZIP: 22314-3187
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LOCATION:
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LOCATION:
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                                                                                             FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
  US/09/526,098
                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 1411 base pairs TYPE: nucleic acid STRANBEDNESS: not relevant
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Matches 370; Conservative
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MOLECULE TYPE: peptide
  APPLICATION NUMBER:
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LOCATION:
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US-09-526-098-11
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Sequence 7, Application US/08523894
Patent No. 6136310
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 AACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 creanacreaegrerereneecececececececererrarracrerecenerar--- 357
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APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heavy chain variable and constant gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1404;
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                                                                                                                                                                                                                                                                                                                                     CAPTER 223.4-316/
CAPTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC Compatible
OPERATING SYSTEM: PC-0DS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NORMER: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIFICATION ** O6-SEP-1995
CLASSIFICATION ** O6-SEP-1995
CLASSIFICATION ** O6-SEP-1995
TERECOMMULICATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 31,030
RECISTRATION NUMBER: 31,030
RELECOMMULICATION INFORMATION:
TELEPHONE: 7703-836-6620
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Pred. No. 6.8e-78;
0; Mismatches 67;
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ropology: linear
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                                358 ATATTGAAATATCTTCACTGGTTATTATACTGGGGCCAGGGAGTCCTGGTCACCGTCTCC 417
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361 GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTTCC
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                                                                                                  US-08-523-894-9

Sequence 9, Application US/08523894

Sequence 9, Application US/08523894

Patent No. 6136310

GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 299.8; DB 3; Length 1 Pred. No. 6.8e-78; 0; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: A LEW. TO LOOS / MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-2620
TELEPHONE: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                    STAIL.
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"WEDIUM TYPE: Floppy disk
"WETER: IBM PC compatible
"VetEM: PC-DOS/MS-DOS
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83.5%;
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 83.5
Matches 353; Conservative
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TCA 420
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MOLECULE TYPE: I
ORIGINAL SOURCE:
                                                                       TCA 423
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LOCATION:
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US-08-523-894-9
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181 CCAGGGAAGGACTGGAGTGGATCGGCTACATCTATGGCAGTGGTGGTGGCGCCCCACCAATTAC 240
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                                                           121 TGCGCTGTCTCTGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                          301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGCCGTGTATTACTGTGCCAGAGATTGG 360
61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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APPLICANT: Newman, Roland A.
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell B.
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHROMOSOME/SEGMENT: heavy chain gamma 4 with the P CHROMOSOME/SEGMENT: mutation
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SOFTWARE:
SOFTWARE:
PALCATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTONREY/AGBRT INFORMATION:
NAME: TESEKIN: Robin L.
REGISTRATION NUMBER: 35,030
REFRENCE/DOCKET NUMBER: 35,030
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street CITY: Alexandria STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/08523894
Patent No. 6136310
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
POSITION IN GENOME:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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RESULT 8
US-08-481-869-19
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                                                                                                                                                                                                                                                                                                                                             TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC 180
                                                                                                                                                                                                                                                                                                                                                                              TGCAGTGTCTCTGGTGGCTCCATCAGCGGTGACTATTATTGGTTCTGGATCCGCCAGTCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGGGAAGGGACTGGAGTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAACTAC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACCCGTCCCTCAAGAGTCGAGTCATCTTTCACAAGACACGTCCAAGAACCAGTTCTCC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358 ATATTGAAATATCTTCACTGGTTATTATACTGGGGCCAGGGAGTCCTGGTCACCGTCTCC 417
                                                                                                                                                                                                                         GIGCAGCIGCAGGAGICGGGCCCAGGACTGGIGAGAGCCTICGGAGACCCTGTCCCTCACC
                                                                                                                                                                                                   1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
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                                                                                                                                                                  Gaps
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Sequence 19, Application US/08379072A
Fatent No. 5658570
GENERAL INFORMATION
APPLICANT: HANNA, Nabil
APPLICANT: RAAB, Ronald W.
TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STREET: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                3;
                                                                                                                               Length 1404;
                                                                                                                                                                67; Indels
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APPLICATION NUMBER: US/08/379,072A
FILING DATE: 25-JAN-1995
CLASSIFFCATION: 424
                                                                                                                             Score 299.8; DB 3;
Pred. No. 6.8e-78;
                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                         70.9%;
83.5%;
                                                                                                                                               Best Local Similarity 83.5
Matches 353; Conservative
                                                         mat_peptide
                       1..1404
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CLASSIFICATION:
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TCA 420
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NAME/KEY:
LOCATION:
FEATURE:
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                                                       , NAME/KEY:
; LOCATION:
US-08-523-894-11
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Fatent No. 5693780
GENERAL INFORMATION:
APPLICANT: NEWMAN, Roland A.
APPLICANT: HANNA, Nabil
APPLICANT: RAAB, Ronald W.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 298.2; DB :
Pred. No. 1.3e-77
0; Mismatches 68
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P.O. Box 1404
                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-UL-1991
ATTORNEY/AGENT INFORMATION:
                        UMBER: US 07/856,281
23-MAR-1992
                                                                                                                                                                           NAME: Rea, Teresa Stanek
REGISTATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 0127)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
US-08-379-072A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 83.2%;
Matches 352; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
PRIOR APPLICATION DATA
APPLICATION NUMBER:
FILING DATE: 23-MAF
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CCAGGGAAGGGACTGGATTGGACGTATCTCTCTGGTAGTGGTGGGCCCACCAACTAC 240
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                                                                                                                                                                                                            APPLICANT: NEWMAN, Roland A.
APPLICANT: HANNA, Nabil
APPLICANT: RAAB, Ronald W.
IITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
NUMBER OF SEQUENCES: 16
CORRESPONDENCE SIDERSS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,237
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 70.5%; Score 298.2; DB 1; Best Local Similarity 83.2%; Pred. No: 1.3e-77; Matches 352; Conservative 0; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-133
TELECOMMUNICATION INPORMATION:
TELEPHONE: (703) 836-6620
                                                                                                      US-08-476-237-15
; Sequence 15, Application US/08476237
Partent No. 5756096
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     423 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
EDNESS: single
TCA 423
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                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CARRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,869
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 298.2; DB 1;
Pred. No. 1.3e-77;
0; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Rea, Teresa Stanek
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 012712-067
RELECHONICATION INFORMATION:
TELEPHONE: (703) 836-620
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 Asse pairs
LENGTH: 423 Asse pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                         CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/379,072A
FILING DATE: 25-JAN-1995
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
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  : Virginia
RY: United States
22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 70.5
Best Local Similarity 83.2
Matches 352; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 CCAGGGAAGGGACTGGAGTGGATCGGCTACATCTATGGCAGTGGTGGGGGGCACCAATTAC 243
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                                                                                                                                                                                                                                                                                         4 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCCCCCAGATGGGTCTTGTCCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 TGCAGTGTCTCTGGTGGCTCCATCAGCGGTGACTATTATTGGTTCTGGATCCGCCAGTCC
                                                                                                                                                                                                                                                                                                                                                                                    64 GTGCAGCTGCAGGAGGCGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 AACCCGTCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
CORRESPONDENCE: 114
                                                                                                                                                                 Length 420;
                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/OR/**
                                                                                                                                                                 DB 1;
                                                                                                                                                            Score 295.2; DB .
Pred. No. 9.8e-77
0; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGT
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I: 699 Prince St.
Alexandria
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APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
FRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 107, Application US/08476349A Patent No. 5750105
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                               69.8%;
83.1%;
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                                                                                                                                                                 Query Match
Best Local Similarity 83.1
Matches 349; Conservative
                                                                    mat_peptide
61..420
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                      4..420
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                   FEATURE:

NAME/KEY: III

LOCATION: 4

LOCATION: 6

LOCATION: 6

US-08-478-039-107
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  NAME/KEY:
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                                                                                                                     304 CTGAAACTGAGGTCTGTGACCGCCGCGGACACGGCCGTCTATTACTGTGCGAGTAAT--- 360
                                                                                                                                                                 361 GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCC 420
                                                                                                                                                                                                             361 ATATTGAAATATCTCACTGGTTATTATACTGGGGCCAGGGAGTCCTGGTCACCGTCTCC 420
                          244 AATCCCTCCCTCAACAATCGAGTCTCCATTTCAATAGACACGTCCAAGAACCTCTTCTCC 303
                                                                    CTGAACCTGAACTCTGTGACCGCGCGGACACGCCGTGTATTACTGTGCCAGAGTTGG 360
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039 FILING DATE: 07-UN-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072 FILING DATE: 25-JAN-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REPERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 107, Application US/08478039
Patent No. 5681722
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
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POSITION IN GENOME:
CHROMOSOME/SEGMENT: Anti-CD4 VH
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: not relevant
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ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 base pairs
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CITY: Alexandria
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STRANDEDNESS: not
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TCA 423
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ORIGINAL SOURCE:
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US-08-478-039-107
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DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                          ZIP: 22314-3187
COMPUTER READABLE FORM:
  TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                            Alexandria
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                                                                                                                                                            USA
                                                                  ADDRESSEE:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 AATCCCTCCTCAACAATCGAGTCTCCATTTCAATAGACGTCCAAGAACCTCTTCTCC 303
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Patent No. 6136310
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 420;
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83.1%; Pred. No. 9.8e-77;
iive 0; Mismatches 68
APPLICATION NUMBER: US 07/856,281
FILING DATE: 33-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTONNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REFERENCE/DOCKET NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEPHONE: 703-836-2021
INFORMATION FOR SEQ 1D NO: 107:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: not relevant
TOPOLLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                    LENGTH: 420 base pairs
IYPE: nucleic acid
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Matches 349; Conservative
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US-08-476-349A-107
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LOCATION:
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                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 83.1%; Pred. No. 9.8e-77,
Matches 349; Conservative 0; Mismatches 66
E: BURNS, DOANE, SWECKER & MATHIS 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, RObin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECHONE: 703-836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
                                                                                                                                                                                                                                                                                             405
                                                                                                                                                                                              301 CTGAACTTGAATTCTGTGACCGACGCGACACGGCCGTCTATTACTGTGCGAGAGGCCCT 360
                                                                                                                                                301 CTGAACCTGAACTCTGTGACCGCCGCGCGCACACGGCCGTGTATTACTGTGCCAGAGATTGG 360
                                                                                                                                                                                                                                                                                                                                                             361 cececrearrecacaacearrrerrarecececrecercearereresececeseaee 420
   241 AACCCGTCCACAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC 300
                                                                    241 AATCCCTCCTCAAGAGTCGAGTCACCATTTCAAAAGACACGTCCAAGAACCAGTTCTTC
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Pred. No. 9.7e-76;
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APPLICATION NUMBER: US/09/526,098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSES: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIPTCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01271
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
INFORMATION FOR SEQ 1D NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09526098 Patent No. 6492134 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 CTGGTCACCGTCTCTCA 438
                                                                                                                                                                                                                                                                                                                                                                                                                                             406 CTGGTCACCGTCTCTCA 423
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TYPE: nucleic acid
STRANDEDNESS: not relevant
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81.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
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Best Local Similarity
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NAME/KEY:
LOCATION:
FEATURE:
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, LOCATION:
US-09-526-098-3
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                                                                                                                                                                                                                                                                                                                               Anderson, Darrell R.
VENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
VENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
VENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAGGGAGGGACTGGAGTGGATTGGCCATATTTATGGTAATGGTGCGACCACCAACTAC 240
361 ATATTGAAATATCTTCACTGGTTATTATACTGGGGCCAGGGAGTCCTGGTCACCGTCTCC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Argaacaccrerederretrecrerecresrescaecreceasaressreserereres 60
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COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EM PC compatible
COMPUTER: EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: U7-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, ROBIN I.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
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Pred. No. 9.7e-76;
0; Mismatches 66;
                                                                                                                                                                                                                                                                                                                           APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONCLONAL ANTIBOD
TITLE OF INVENTION: "PO HUMAN B'.1 AND/OR B'.2
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                          US-08-487-550-3
; Sequence 3, Application US/08487550
; Patent No. 611388
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid STRANDEDNESS: not relevant
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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ilarity 81.5%;
Conservative
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Best Local Similarity
Matches 357; Conserva
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LOCATION:
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LOCATION:
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                                                               1 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
                                                                                                                               9
                                                                                                                                   1 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
Gaps
15;
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Baughn, Mariah R.
APPLICANT: Baughn, Mariah R.
APPLICANT: Baughn, HIWAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ee; Indels
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FSSLENG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/09049672A Patent No. 6135941
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   Matches 357; Conservative
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Pred. No. 6.5e-75;
0; Mismatches 49
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                                                                               INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1567 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                             68.5%;
85.9%;
                    TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
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; CLONE: 1513264
US-09-049-672A-17
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Matches 371; Conserv
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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	December 29, 2003, 16:08:50 ; Search time 1603.14 Seconds (without alignments) 9875.644 Million cell updates/sec	US-09-019-441-3 387 1 ATGGACATGAGGTCCCCGCGGACCAAGGTGGAAATCAAA 387	
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ısing sw	2003, 16	-3 JGTCCCCG	sapext 1
cleic search, u	December 29, 2	US-09-019-441-3 387 1 ATGGACATGAGGG	IDENTITY NUC Gapop 10.0 , Gapext 1.0
OM nucleic - nucleic search, using sw model	Run on:	Title: Perfect score: Sequence:	Scoring table: IDENTITY NUC Gapop 10.0

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

2888711 seqs, 20454813386 residues

Searched:

5777422

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Embl:* gb_ba:* gb_htg:* gb_in:* gb_om:*	b pat: * * * * * * * * * * * * * * * * * * *	gb_ro:* gb_sts:* gb_sy:*	gb_v:: em_ba:: em_fun:: em_fun::		em_pat:* em_ph:* em_pl:* em_ro:* em_sts:*
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Database :					

Pred. No. is the number of results predicted by chance to have a

em\_htg\_hum:\*
em\_htg\_hum:\*
em\_htg\_other:\*
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em\_htg\_pln:\*
em\_htg\_pln:\*
em\_htg\_pln:\*
em\_htg\_pur:\*
em\_htg\_mam:\*
em\_htg\_wam:\*
em\_htg\_vd:\*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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No.	Score	Z Z	Leng	DB	ΩI	Description
1	387	100.0	1904	9		BD075127 Method fo
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æ		88.4	a	9	BD090625	0
4		88.4	729	9	96	6 Humaniz
ស		88.0	388	σ	HSA548508	ŝ
9		86.4	390	σ.	ເດ	Macaca
7		86.4	396	9		8 Human mR
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10			406	σ	HUMIGKFAN	Human r
11			400	σ	AF228327	Homo
12	~	85.5	962	σ	BC034141	BC034141 Homo sapi
. 13	330.8	85.5	432	0	HUMIGKVCA	L01279 Homo sapien
14	329.4	85.1	390	σ	MMU57579	æ
15	329.4		974	9	AX305000	0
16	329.4		974	ø	AX306529	53
17	329.4	85.1	974	ø	BD131246	46
18	328.4	84.9	370	σ	HSIGKLV20	Ξ
19	326.2	84.3	396	σ	HSPBLIGVD	Ξ.
20	326.2	84.3	714	9	AX616570	0 Sequence
21	325.6	84.1	383	6	HSIGKLV56	H.sapie
22	324.6	83.9	430	σ	AF417853	3 Ношо
23	324.6		448	φ	BD182345	s :
24	323.6	83.6	389	σ	HSIGKLV06	÷.
25	323	83.5	728	φ	AX327729	29 Sequ
26	323	83.5	728	9	BD182353	53 Anti CD4
27	321.4	83.0	388	σ	HSTROIGVJ	H.sapiens
28		83.0	390	σ	HSFOG1L	X64163 H.sapiens m
29	٠.	83.0	441	σ	HSU43767	귶
30		83.0	- 716	9	7	٠,
31	321.2	٠	650	თ	HSA010446	AJ010446 Homo sapı
32		82.5	399	σ	HSIGKLV23	ı.
33			388	9	AR161375	'n
34			388	ø	BD096602	2 Trans
35			926	σ	BC029444	4
36	_		390	σ	HSU43773	773 Human
37	14.	81.3	369	0	HSIGKLV02	•
38	-		395	0	HSIGKLV41	462 H
39	13.	81.0	388	σ	HSDELIGVJ	95 H.sapiens
	13		388	σ	HSTREIGVJ	996 H.sapie
	13	81.0	427	9	BD182339	2339 Anti
	m		427	9	BD182341	D182341 Anti
43	Н	81.0	953	σ	BC005332	05332 Homo
44	m		388	σ	HSIGKLV58	479 H.sapie

## ALIGNMENTS

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REFERENCE
AUTHORS
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Homo sapiens immunoglobulin light chain variable region (IGL@)
M74019
via homologous recombination and vectors for accomplishing the same
Patent: JP 2001516221-A 3 25-SEP-2001;
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                                                              PN JP 200151621-A/3
PD 25-SEP-2001
PP 25-SEP-2001
PP 25-SEP-2001
PR 14-MAR-1997 US 08/819866,13-FEB-1998 US 09/023715 PI
MITCHELL E REFF, RICHARD SPENCE BARNETT, KAREN RETTA MCLACHLAN PC C12M15/90, C12M15/90, C12M15/95, C12Q1/68, C12N5/10, C12N9/12, C12M15/13, PC COX16/52, C12M15/12, C07X14/705, G01N33/53, C12N15/62, C07X16/90, CC Strandedness: Single;
CC Topology: Linear;
CC Method for integrating genes at specific sites in mammalian CC method for integrating and vectors for accomplishing the CC homologous recombination and vectors for accomplishing the
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Method for integrating genes at specific sites in mammalian
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/organism='Unidentified'
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/db_xref="taxon:32644"
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Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Homo sapiens (human) M74019.1 GI:186042

VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

ACCESSION

```
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 429)
Silbersteini, L.B., Jefferies, L.C., Goldman, J., Friedman, D.,
Moore, J.S., Nowell, P.C., Roelcke, D., Pruzanski, W., Roudier, J. and
Silverman, G.J.
Variable region gene analysis of pathologic human autoantibodies to
the related I and I red blood cell antigens
Blood (1991) In press
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon start=1
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/brotein id="AAAS9100.1"
/brotein id="Is66043"
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CRASQSISSYLNWYQQKPGKAPKILIYAASSLQSGVPSRFSGGGGGTDFTLTISSLQP
EDFATYYCQQSYSTPWTFGQGTKVEIKRTVAAPSVFIFPPS"
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/gene="IGL@"
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Drug containing humanized anti-Fas antibody.
BD090625
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                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="22"
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Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                     3/12,
A61P19/02,A61P29/00,A61P37/00,A61P37/06,A61P37/08,A61P43/00//
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                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini: Hominidae; Homo.

Lobaes 1 to 729;
Serizawa,N., Haruyama,H., Nakahara,K. and Tamaki,I.

Brug containing humanized anti-Fas antibody
Drug containing humanized anti-Fas antibody
Sahene: JP 2001342148-A 85 11-DEC-2001;
SANKYO CO LID
OS Homo sapiens (human)
OS Homo sapiens (human)
PD 11-DEC-2001
PF 28-MAR-2001 JP 2001093106
PF 28-MAR-2001 JP 2001093106
PF 1 NOBUFUSA SERIZAWA,HIDEYUKI HARUYAWA,KAORI NAKAHARA,IKUKO PI
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A61K37/02,C12N15/00
Drug containing humanized anti-Fas antibody
Key Location/Qualifiers
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JP 2001342148-A/85.
Homo sapiens (human)
Homo sapiens
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PC C1
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PAT 31-JAN-2002

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DEFINITION ACCESSION VERSION KEYWORDS

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Homo sapiens partial mRNA for immunoglobulin light chain variable region (IGLV gene), clone RN86.
AJ548508.
IGLV gene; immunoglobulin light chain variable immunoglobulin light chain variable region.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                NOBUKI SERIZAWA, HIDEYUKI HARUYAMA, KAORI NAKAHARA, IKUKO TAMAKI CI2N15/09, A61K39/00, A61K39/395, A61K39/395, A61P37/02, A61P43/00, C07K16/18, C12N1/21, C12N5/10, C12N1/0, (C12N1/21, C12R1:19), C12N15/00, PC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 729)
Serizawa, N., Haruyama, H., Nakahara, K. and Tamaki, I. Humanizad anti-Fas antibody Patent: JP 2000166574-A 85 20-JUN-2000;
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Pred. No. 6.1e-101;
0; Mismatches 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
_200 c 182 g 155
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                                                                                                                                                                                            Homo sapiens (human)
JP 2000166574-A/85
20-JUN-2000
29-SEP-1999 JP 1999275441
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Best Local Similarity 92.8%;
Matches 359; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="immunoglobulin light chain variable region"
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/db_xxef="d1:28611057"
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EDFATYYCQQSYSTPRTFGQGTKVEIR"
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Potentially disease-modifying effects of apoptotic-cell specific immune responses
immune responses
1 (Dipublished
2 (Dipublished
2 (Direct Submission)
Pal,R.
Direct Submission
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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/gene="IGLV"
/product="immunoglobulin light chain variable region"
106 c 96 g 88 t
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Pred. No. 2e-100;
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                                                                                                                                                                                                                                                                                                                                                               1. 388
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/gene="IGLV"
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Best Local Similarity 92.5%;
Matches 358; Conservative
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/gene="IGLV"
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/pranslation="MONRABLTGLLKR"

BDFATYYCLQYNSDPFTFGPGTKLDIKR"

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ישיוט אפרו 190 bp mRNA linear PRI 02-OCT-199י
Macaca mulatta Ig rearranged light chain variable region, anti-RBC
antibody, mRNA, partial cds.
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Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Blancher,A.and Capra,J.D.
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2 (bases 1 to 390)
Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A. and Capra, J.D.
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Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
University of Texas Southwestern Medical Center, 6000 Harry Hines
Blvd., Dallas, TX 75235-9140, USA
Location/Qualifiers
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Pred. No. 2.5e-98;
0; Mismatches 33; Indels 0
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/mol_type="mRNA"
/db_xref="taxon:9544"
/note="hybridoma 1D8"
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Best Local Similarity 91.5%;
Matches 354; Conservative
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BD015544 linear PAT 27-AUG-2002 Human monoclonal antibody against TGF-beta-II receptor and medicinal use thereof.
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1 (Dases 1 to 438)

Sakamoto, S. and Kamada, M.

Human monoclonal antibody against TGF-beta-II receptor and medicinal use thereof

Patent: JP 2001206899-A 6 31-JUL-2001;

JAPAN TOBACC IV.

OS Homo sapiens (human)

PN JP 2001206899-A/6
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C12N5/10,C12N15/02//C12P21/08
Human monoclonal antibody against TGF-beta-II receptor and
medicinal use
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08-NOV-2000 JP 2000340216
SHINJI SAKAMOTO,MASAFUMI KAWADA
CO7K16/28,A61K39/395,A61P1/16,A61P9/04,A61P9/10,A61P9/10,
121 GTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG
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                                                         181 AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
_123 c 111 g 101
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JP 2001206899-A/6.
Homo sapiens (human)
Homo sapiens
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PC CO7K16
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PC A61P12
PC A61P42
PC C12N5/
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1 (Dasea I to 386)
1 (Dasea I to 386)
Amino Acid Sequence of Anticancer Human Monoclonal Antibody And DNA Amino Acid Sequence Coling For THE SAME
BASE SEQUENCE COLING FOR THE SAME
PATENT: JP 1997100300-A 2 15-APR-1997;
                                                         E12918 197-APR-1998 Human mRNA for variable region of light chain of anti-carcinoma monoclonal antibody CLN''1-IgM, complete cds.
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region (CDR1)'
214. .334
/note='this region encodes Complementarity
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/note='this region encodes Complementarity
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Location/Qualifiers
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region (CDR2)'
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91.5%;
                                                                                                                  E12918.1 GI:3251749
                                                                                                                             JP 1997100300-A/2.
Homo sapiens (human)
Homo sapiens
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Matches 354; Conservative
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1. (Dasses 1 to 438)
Sakamoto,S. and Kamada,M.
Human monoclonal antibody for human TGP-beta type II receptor and pharmaceutical use thereof
L. Patent: WO 0136642-A 6 25-MAY-2001;
DAPAN TOBACCO INC,SHINJI SAKAMOTO,MASAFUMI KAMADA
OS Homo sapiens (human)
PN WO 0136642-A/6
PD 25-MAY-2001
PF 17-NOV-2000 WO 2000JP008129
PR 18-NOV-1999 JP 99P 328681,08-NOV-2000 JP 00P 340216 PI
SHINJI SAKAMOTO,MASAFUMI KAMADA
PC CIZNIS/13,CO7K16/28,CIZNIS/16,A6IK39/395,A6IP43/00,A6IP13/12,PC
A6IP11/00,
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Human monoclonal antibody for human TGF-beta type II receptor and
physmaceutical use thereof.
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GTCACCATCACTTGCAGGCCAAGTCAGGACATTAGGTATTTAAATTGGTATCAGCAG
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AGIP1/16,AG1P9/08,AG1P9/10,AG1P17/06,AG1P17/04,AG1P17/02,
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M87478.1 GI:185950

C-region; J-region; V-region; immunoglobulin kappa-chain; immunoglobulin light chain.
Homo sapiens (human)
Homo sapiens (human)

E ukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 406)

Aucouturier, P., Bauwens, M., Khamlichi, A.A., Denoroy, L., Spinelli, S., Touchard, G., Preud'homme, J.L. and Cogne, M.
Monoclonal Ig L chain and L chain W domain fragment crystallization in myeloma-associated Fanconi's syndrome

L J. Immunol. 150 (8 Pt 1), 3561-3568 (1993)
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EDFATYYCQQSYSIPWTFGQGTKVEIKRTVAAP"
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Location/Qualifiers
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/gene="IgK"
56...>406
/gene="IgK"
/product="immunoglobulin kappa chain"
56...388
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Human rearranged IgK mRNA VJC region.
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/isolate="tpatient CHEB"
/ib xref="teaxon:9606"
/map="2p12"
/map="zp12"
/tissue type="plasma"
/tissue type="bone marrow"
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Homo sapiens clone BUS immunoglobulin light chain variable region
                                  "note="This CDS feature is included to show the translation of the corresponding C_region. Presently translation qualifiers on C_region features are illegal." | proteIn_id="AAAS1020.1" | proteIn_id="AAAS1020.1" | proteIn_id="RVAAP" | the xref="GI:561655" | translation="RTVAAP" | 1899. . > 406
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I (bases 1 to 400)
Maloum, K., Dighiero, G. and Magnac, C.C.
Unmutated Ig VH genes in CLL patients
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Pred. No. 8.5e-98;
0; Mismatches 34.
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Maloum, K., Dighiero, G. and Magnac, C.C.
Direct Submission
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/mol_type="genomic DNA"
/note="V1-J1 region"
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/protein id="AAPR6916.1"
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DRATYOGSYSTPRIFGGGTKVEIKHRAR"
a 109 c 100 g 92 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 TCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAG 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 ACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTTAAATTGGTATCAGCAGAAA 183
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                                                                                                                  /note="isolated from B-cell chronic lymphocytic leukemia
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Homo sapiens, similar to anti TNF-alpha antibody light-chain Fab
fragment, clone MGC:32713 IMAGE:4691280, mRNA, complete cds.
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Direct Submission
Submitted (02-JUJ-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGGTGCCAGA
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/product="immunoglobulin light chain variable region"
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                                                                                       /rearranged
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Mammalia, Eutheria,
1 (bases 1 to 962)
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/map="2
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                                                                            RESULT 13
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                         셤
NIH-MGC Project URD: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbar-remail.nih.gov
Tissue procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 41 Row: j Column: 19 This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MDMRVPSQLIGHLILMLPGARCDIQLTQSPSFLSASVGDRVTITTRASGLISSYLAWYQQKPGKAPNLIYAASTLQSGVBSRFSGSGSGTBFTLTISSLQPPBPATYYCQQLNSSPPTFGGGTKVEIKRTVAAPSVFIPPPSDEQLKSGTASVCLLINNFYPREAKVQWKVDNALQSGNSGESYTEQDSKBSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26. .736
/codon_start=1
/product="similar to anti TNF-alpha antibody light-chain
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Pred. No. 3e-97;
n. Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="MGC:32713 IMAGE:4691280"
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/clone_lib="NIH MGC_77"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAH34141.1"
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                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Best Local Similarity 91.0%;
Matches 352; Conservative
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HUMIGKVCA 432 bp mRNA linear PRI 05-MAY-2000
HOmo sapiens immunoglobulin kappa light chain VC region (IGK) mRNA,
partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MDMRVPAQLLGLLLLMLRGARCDIQMTQSPSSLSASVGDRVTIT
CRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQP
EDFATYYCQQSYSTPPWTFGQGTKVEIKRTVAAPSVFIFPPS"
                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 432)

Friedman, D.F., Moore, J.S., Erikson, J., Manz, J., Goldman, J., Nowell, P.C. and Silberstein, L.B.
Variable region gene analysis of an isotype-switched (IgA) variant of chronic lymphocytic leukemia
Blood 80 (9), 2287-2297 (1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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/protein iaAAA59089.1"
/db_xref="GI:185985"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /ceil_type="lymphoblast"
/tissue_type="chronic lymphocytic leukemia blood"
/dev_stāge="adult"
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Pred. No. 3.3e-97;
0; Mismatches 27;
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/db_xref="taxon:9606"
/map="2p12"
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/gene="IGK"
/note="G00-119-341"
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0y         121 GTCACCATCACTTGCAGGCAAGTCAGGACATTAGGTATTATAATTGGTATCAGCAG           0b         121 GTCACCTTCACTTGCAGGCCAAGTGAGAACGTTAACAATTACATTAGATTGGTATCAGCAG           0y         181 AAACCAGGAAAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC           0y         241 CCATCAAGGTCCTGATCTATGGTGCATCCACTTTGCAAAGTGGGGTC           0y         241 CCATCAAGGGAATGGATCTGGTGCATCACTCTCACCTTGCACAGTGGGGTC           0y         241 CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTCACTCTCACCGTCAGCAGCTG           0y         301 CAGCCTGAAGTTCAGCGGCAGTGGATCTTATACTGTTCACCTCTCACCATCAGCAGCTG           0y         301 CAGCCTGAAGTTTATACTGTCTACAGGTTTATAGTACCCTCCAGCAGCTTCTTCCACCATCAGAAGTTTTTCACTCTCACCATCAGAAGTTTTTTTT	36	AUTHORS Takashi,T., Katsunari,T.P. and Nobuaki,H.  TITLE Human monoclonal antibody against a costimulatory signal transduction molecule alilm and pharmaceutical use thereof JOURNAL Patent: EP 1158004-A 29 28-NOV-2001;  FEATURES Location/Qualifiers  Location/Qualifiers    Apan Tobacco Inc. (JP)	=1 (-AD19026.1" :17644679" =17644679" =1700KPROLLGLLILWFPGS WYQOKPGKAPKLLITYVASSLQS SPWTFGGOTKVEIKTVAAPS DNALQSGNSQESVTEQDSKDST FNRGEC" 232 g 214 t	Query Match         85.1%;         Score 329.4;         DB 6;         Length 974;           Best Local Similarity         90.7%;         Pred. No. 1e-96;           Matches 351;         Conservative         0;         Mismatches 36;         Indels         0;         Gaps           Qy         1 ATGGACATGAGGGTCCCGGTCAGGTCCTGGGGCTCCTTCTGCTCTGGTTCCCAGGTGCC         Db         39 ATGGACATGAGGGTCCCCGCTCAGCTCTGGGGCTCCTGCTGCTGCTCTGGTTCCCAGGTTCC         The standard Control of the standa	Oy 61 AGATGTGACATGACCCAGTCTCCATCTTCCCTGTCTGTAGGGGACAGA
0y         181 AAACCAGGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC 240           Db         181 AAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCTACCAGTTTGCAAAGTGGGGTC 240           Oy         241 CCATCAAGGTCAGTGGATCTGGGACAGATTCACTCTCACCGTCAGCAGCTG 310           Db         241 CCATCAAGGTCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGTTG 310           OY         301 CAGCCTGAAGATTTGCGACTTATTACTGTCTACAGGTTTATAGTACCTCTCACCATCAGCAGTTG 310           OY         301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCCACCAGACG 350           Db         301 CAGCCTGAAGATTTTGCAACTTACTACTGTCTACAGGTTACAGTACCCCCCCTGGACG 360           OY         358 TTCGGCCAAGGGACCAAGGTGGAAATCAAA 387           Db         351 TTCGGCCAAGGGACCAAGGTGGAAATCAAA 390           361 TTCGGCCAAGGGACCAAAGGTGGAAATCAAA 390	MRUS7579 MACCESSION WS7579.1 GI:1575105 MSEXMORDS MACACA mulatta (rhesus monkey) MRAMALA: Mataca mulatta (rhesus monkey) MATHORS MATHORS MACACA: Mataca mulatta (rhesus mataca mulatta (rhesus mataca mulatta (rhesus monkey) MATHORS MATHORS MACACA: Mataca mulatta (rhesus mataca mulatta (rhesus monkey) MATHORS MATHORS MACACA: MACACA (rhesus monkey) MATHORS MATHORS MACACA: MACACA (rhesus monkey) MATHORS MATHORS MACACA (rhesus monkey) MATHORS MACACA (rhesus monkey) MATHORS MACACA (rhesus monkey) MATHORS MACACA (rhes	TITLE Variable Region Gene Segment Utilization in Rhesus Monkey Hybridomas Producing Human Red Blood Cell-Specific Antibodies: Predominance of the VH4 Family but not VH4-21 (V4-34) JOURNAL Unpublished AUTHORS Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Blancher,A. and Capra,J.D.  TITLE Direct Submission JOURNAL Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center, University of Texas Southwestern Medical Center, 6000 Harry Hines Blvd., Dallas, TX 75235-9140, USA Blvd., Dallas, TX 75235-9140, USA Source 1. 390 1. 390	/organism="Macaca mulatta" /mol_type="mRNA" /db_xref="taxon:9544" /noTe="hybridoma 1G7" 1390 /codon start=1 /product="immunoglobulin light chain" /product="immunoglobulin light chain" /product="immunoglobulin light chain" /proctein id="AAB09456.1" /db_xref="G1:1575166" /translation="MDMRAPAQLIGLLLIMLPGARCDIQMTQSPSSLSASVGDRVTFT /translation="MDMRAPAQLIGLLLIMLPGARCDIQMTQSPSSLSASVGDRVTFT CRASENVENYLHWYQQKPGKAPKLLIYGASTLQSGVPSRFSGSGSGTDFTLTISSLQP EDVATYCQHSYGGTPLFGGGTVPIRR" BASE COUNT 94 a 110 98 b	tch al S 351	Db 1 ATGGACATGAGGCCCCGGTCAGGCTCCTAGGCTCCTGCTCTGCTCCTGCTCCCAGGCGCC 60  Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATGTTCCCTGTCTGCATCTGTAGGGGACAGA 120

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159 GTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGGTTGTTAGCCTGGTATCAGCAG 218
                                                                        219 AAACCAGGGAAAGCCCCTAAACTCCTGATCTATGTTGCTGCATCCAGTTTGCAAAGTGGGGTC 278
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Search completed: December 29, 2003, 19:01:27 Job time : 1605.14 secs

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Database

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 493)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

LUpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov/

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

CLONG distribution: M.G. Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llni.gov/bbrp/image/image.html

Seq primer: M13 Forward.
CB984750 AGENCOURT
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UI-HF-BLO-abp-a-02-0-UI.rl NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3057290 5', mRNA sequence.
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                           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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MAGE:30354121 5', mRNA sequence.
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
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/cnost="vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
/cnost-ucted from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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Email: cgapbs-romail.nih.gov
Tissue Procurement: Dr. Michel Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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NIH-WGC http://mgc.noi.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                           88.7%; Score 343.4; DB 9; Length 93.2%; Pred. No. 6.6e-92; ive 0; Mismatches 26; Indels
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Mammalia, Eutheria, Primates,
1 (bases 1 to 923)
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/clone=lib="NIH_M
                                                                                                                                                                                       Email: crapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (Linl.)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCMISS row: p column: 02
High quality sequence stop: 549.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases: 1 to 724)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
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AGENCORT_8616470 NIH_MGC_113 Homo sapiens CDNA clone IMAGE:6302159
BO882857
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Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapDs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can by
ttp://image.llnl.gov
tolumn: 24
High quality sequence stop: 672.
Location/Qualifiers
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Pred. No. 6.4e-91;
0; Mismatches 29;
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1. .969
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TITLE
JOURNAL
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KEYWORDS
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/lab host="Dhids Tiphage-resistant"
/lab host="Dhids Tiphage-resistant"
/clone lib="NH MGC 184"
/clone lib="NH MGC 184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
Sfil (ggccattatggcc); Site_2: Sfil (ggccgcctcggcc);
Library is oligo-dr primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyoid,
parathyroid, adrenal, cortex and pineal gland. S' and 3'
adaptors were used in cloning as follows: S' adaptor
sequence: S'-CACGCGACATTATGGCC.3' and 3' adaptor sequence:
S'-ATTCTAGAGGCCCATATATGGC.3' and 3' adaptor sequence:
S'-ATTCTAGAGGCCATATATGGC.3' and 3' adaptor sequence:
S'-ATTCTAGAGGCCATATATGGC.3' and 3' adaptor sequence:
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
and was constructed by Clonecch Laboratories (Palo Alto,
CA). Note: this is a NHH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: NDCM133 row: k column: 22
                                                                                                                                                                                                                                                                                                                      AGENCOURT 13574990 NIH MGC 184 Homo sapiens CDNA clone IMAGE:30326373 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo... I (bases 1 to 799)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGGTGCC
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Pred. No. 1.8e-90;
0; Mismatches 30; Indels
                                                                            GGCCAAGGGACCAAGGTGGAAATCAAA 387
                                                                                                                      GGCCAAGGGACCGAGGTGGAAATCAAA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 412.
Location/Qualifiers
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92.2%;
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Best Local Similarity 92.2
Matches 357; Conservative
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//db_tref="taxon:9606"
//db_tref="taxon:9606"
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//dlob_host="DH10B (phage-resistant)"
//dlob_host="DH10B (phage-resistant)"
//dlob_host="DH10B (phage-resistant)"
//dlob_host="DH10B (phage-resistant)"
//dlob_host="Organ: spleen; yoctor: pOTB7; Site_1: XhoI; Site_2: BCRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  969 bp mRNA linear EST 17-OCT-2002
5', mRNA sequence.
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1 (Dases 1 to 969)
1 MH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
Contact: Robert Strausberg, Ph.D.
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                                14 ATGGACATGAGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCC
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Tissue produrement: Dr. Mark Watson
Tissue produrement: Dr. Mark Watson
CDNA Library Pepsaration: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can bfound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llh.gov
Plate: LLCM2470 row: h column: 03
High quality sequence stop: 640.
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/note="
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Tissue Procursement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL.)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
ROMIN COLUMN: 20
High quality sequence stop: 408.
High quality sequence stop: 408.
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                                                                                                                                         134 GTCACCATTACTTGCCGGGCAAGTCAGGGCATTAGCAATGATTTAGGCTGGTATCAGCAG 193
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                              AGATGTGCCATCCAGATGACCCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGA 133
                                                                                                                                                                                                                                                                                     AAACCAGGGAAAGCCCCTAAACTCCTGATCTATGCTGCATCCAGTTTACAAAGTGGGGTC 253
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 769)

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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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CB956923 708 bp mRNA linear EST 29-APR-2003
AGENCOURT 13778921 NIH MGC 184 Homo sapiens cDNA clone
IMAGE:30351494 5', mRNA sequence.
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Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
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/clone lib="NIH MGC 184"
/note="Organ: Pooled-clandular; Vector: pDNR-LIB; Site_1:
Sfil (ggccattatggc); Site_2: Sfil (ggccgctcggcc);
Library is oligo-dT primed and directionally cloned. CDNA
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1 (bases 1 to 708)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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     Length
                                                            Indels
  DB 14;
Score 337.4; DB 1-
Pred. No. 5.3e-90;
0; Mismatches 31
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/db_xref="taxon:9606"
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     87.2%;
92.0%;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 745)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits CDNA Library Preparation: CLONTECH Labbratories, Inc.

CDNA Library Preparation: CLONTECH Labbratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bisocience Corporation

Clone distribution: MGC clone distribution information can be thtp://image.llnl.gov

http://mage.llnl.gov

Plate: NDCM151 row: i column: 18

High quality sequence stop: 557.
was prepared from a glandular pool of tissues from thyoid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGACATG-GT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average innert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clonech Laboratories (Palo Alto, CA). Note: this is a NIH MGC Library."
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                                                                                                                                                                                                                                                              DB 14; Length 708;
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AGENCOURT 13784991 NIH MGC_184 Homo sapiens cDNA clone
IMAGE:30352433 5′, mRNA sequence.
                                                                                                                                                                                                                                                                                                    32; Indels
                                                                                                                                                                                                                                                          Score 335.8; DB 1.
Pred. No. 1.5e-89;
0; Mismatches 32
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91.7%;
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/organlams=nowww.ver-
/moltype="mRNA"
/db xref="taxon:966"
/clone="inAdE:30352433"
/lab_host="hulbB (Tiphage-resistant)"
/lab_host="hulb (Tiphage-resistant)"
/clone lib="Hulb (Tiphage-resistant)"
/clone lib= lib-ary was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA) Note: this is a NIH MGC Library."
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IMAGE:30326564 5', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 763)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Matches 355; Conserv
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COMMENT

FEATURES

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/organism="Homo sapiens"
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/db_xref="taxon:9606"
               GI:30279919
                                              Homo sapiens
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                                                                                                                                                                                                                                       Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM34 row: c column: 21
High quality sequence stop: 602.
Location/Qualifiers
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AGENCOURT 13643437 NIH MGC 184 Homo sapiens cDNA clone
IMAGE:30328513 5', mRNA sequence.
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Pred. No. 4.8e-89;
0; Mismatches 33
                                                                                                                                                                                  1. .763
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/clone="IMAGE:3035813"
/lab host="DH10B (T1 phage-resistant)"
/lab host="DH10B (T1 phage-resistant)"
/clone="DH10B (T1 phage-resistant)"
/clone="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
Sfil (ggccattatggcc); Site_2: Sfil (ggccgcctcggcc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyoid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.66-3.5 kb): 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
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CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
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Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGACATG-4T (30) BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
http://image.lln.gov
High quality sequence stop: 577.
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NIH-WGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                 mRNA sequence. ____BG540787
BG540787.1 GI:13533020
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 9106 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence balongs to sequence cluster 1696.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1026DF11QP1&cluster=1696.r. Contact:
Feng Liang Email: fliang@lifetech.com/URL
Feng Liang Email: fliang@lifetech.com/RuvircGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0D1026DF11QP1.
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25-NORMALIZED Homo sapiens CDNA
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Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M. A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M. A.G.E. Consortium/LLNL at:
http://image.llnl.gov
e column: 12
High quality sequence stops: 407.
Location/Qualifiers
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247 AACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGGTCC 306
                                                                             CATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGC 366
                                                                                                                                                        AGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCG 361
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 743)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.B. Consortium/LLNL at:

http://mage.llnl.gov

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IMAGE:30353580 5', mRNA sequence.
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Rammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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29 ATGGACATGAGGGTCCCCGCTCAGGCTCCTTGGACTTCTACTCTGGCTCCCGAGGTGCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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147 GTCACCATCACTTGCCGGGCAAGTCAGGCATTGGAAGTGATTTAGGCTGGTATCAGGCAG 206
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by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH MGC Library."

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Anti-human CD23 5E8 monoclonal antibody light chain variable region DNA.
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Human immunoglobul
Humanised anti-Fas
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Anti-human AILIM m
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                                                                                                                                 (without alignments)
6187.013 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N Geneseq 19Jun03:*

| SIDS1/gcgdata/geneseqn-emb1/NA1980.DAT:*
| SIDS1/gcgdata/geneseqn-emb1/NA1981.DAT:*
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| SIDS1/gcgdata/geneseq-geneseqn-emb1/NA1995.DAT:*
| SIDS1/gcgdata/geneseq-geneseqn-emb1/NA1999.DAT:*
                                                                                                             December 29, 2003, 16:08:50 ; Search time 168.851 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /geneseqn-embl/NA2001A.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /genesegn-embl/NA2001B.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |SIDS1/gcgdata/geneseg/genesegn-embl/NA2001A.DAT
|SIDS1/gcgdata/geneseg/genesegn-embl/NA2001B.DAT
|SIDS1/gcgdata/geneseg/genesegn-embl/NA2002.DAT:
|SIDS1/gcgdata/geneseg/genesegn-embl/NA2003.DAT:
                                                                                                                                                                                               187
1 ATGGACATGAGGGTCCCCGC......GGACCAAGGTGGAAATCAAA
             GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                 2552756 segs, 1349719017 residues
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AAS99473
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AAV61794
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ABL46009
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Gapop 10.0., Gapext 1.0
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Maximum DB seq length: 200000000
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Match 1
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342.2 342.2 332.3 334.2 334.2

Score 387 387

. 8 Result

Functional kappa t Human immunoglobul Nucleotide sequenc Partial nucleotide

Human pancreatic t 93KA9 anti-Varicel

Humanized 1308F VL Hu1308 VL encoding Human IGFAM-13 imm Human dithp antige

Nucleotide sequenc Human immunoglobul Synthetic kappa li Nucleotide sequenc Human colon tumour Kappa light chain

Human anti-RSV mon

Human IGFAM-10 imm Human IGFAM-9 immu Human anti-HBs lig

Nucleotide sequenc Anti-CD40 monoclon Anti-CD40 monoclon

DNA encoding the

Nucleotide sequenç Human immunoglobul Functional Kappa t Partial nucleotide Human IGFAM-1 immu Anti-CD40 monoclon Anti-CD40 monoclon

Human colon cancer Anti-CD40 monoclon

Scoring table:

Searched:

Database

Perfect score:

Sequence:

OM nucleic

Run on:

Human breast cance Nucleotide sequenc Human ovarian anti Human colon tumour

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AAV61794;
              361
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AAV61794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New anti-human CD23 monoclonal antibody - used for inhibiting IgE expression to treat or prevent allergic, inflammatory and
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Best Local Similarity 100.0%; Pred. No. 1.6e-108;
Matches 387; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 387 BP; 92 A; 102 C; 98 G; 95 T; 0 other;
            /tigs e
/note="encodes CDR 2 region"
313.357
/ttsg f
/note="encodes CDR 3 region"
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98US-0019441
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214..234
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/note= "this base represents a nucleotide missing
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OS Chimeric - Cytomegalovirus.

Chimeric - Rhesus macaque polyoma virus.

Chimeric - Photinus sp.

-aric - Photinus sp.
Location/Qualifiers
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This is the nucleotide sequence of novel target plasmid Mandy.

The plasmid includes an inactivated murine dihydrofolate reductase

(DHFR) gene, the Escherichia coll beta-galactosidase gene,

baculovirus DNA, a cassette comprising the promoter and enhancer

elements from cytomegalovirus and SV40 virus, the E. coli

beta-glucuronidase (GUS) gene, firefly luciferase gene, an

inactivated Salmonella typhimurium histidinol dehydrogenase (HisD)

gene and transposon TnS neomycin phosphotransferase (neo) gene

contention provides a novel method for integrating a desired

invention provides a novel method for integrating a desired

invention provides a novel method for integrating a desired

coll via homologous recombination. This involves transfecting the

cell via homologous recombination as Desmond (see Aav61792), which

cell with a 'marker plasmid' such as Desmond (see Aav61792), which

contains a unique sequence that is foreign to the mammalian cell

genome and which provides a substrate for homologous recombination,

followed by transfection with a 'target plasmid', such as Mandy

con Molly (see AAV61793), containing a sequence which provides for

homologous recombination with the unique sequences contained in

the marker plasmid, and further comprising a desired DNA that is

to be integrated into the mammalian cells, typically an

immunoglobulin or other secreted mammalian glycoprotein. The

contains electable marker. The neo gene as a

contained and the marker. The neo gene is split into 3 exons. mammalian cells, and can be used to express any type of recombinant protein. The use of a triply spliced selectable marker means that all selected colonies arise from homologous recombination. In of the targeting vector with the integrated marking vector results in correct splicing of all 3 exons of the neo gene and expression of a functional neo protein. The method is applicable to all Commission between Matrix and the marker plasmid and becomes integrated into the host cell genome upon integration of the marker plasmid into the mammalian cells. Exons I and 2 are present on the targeting plasmid, and are separated by an intron into which at least one gene of interest is cloned. Homologous recombination e.g. addition, the number of colonies that need to be screened to identify high producer clones is reduced. An amplifiable gene be inserted on integration of the marking vector, so that when gene is targeted to this site, the gene is further enhanced by expressing, comprises homologous recombination using specific integration of DNA in mammals for selectable marker and target plasmids Example 1; Fig 10; 114pp; English - sulingo amplification [mmnnog] Site 

Sequence 19035 BP; 4705 A; 4968 C; 4822 G; 4519 T; 21 other;

7600 7721 AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC 7780 ö 120 7601 AGATGTGACATCCAGATGACCCAGTCTTCCTTCTCCTGTCTGCATCTGTAGGGGACAGA 7660 180 7661 Grcaccarcacrrecaececaagrcaesacarraecrariatriraaarrecarrecae 7720 240 09 7541 ArigaAcAridAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCAGGTGCC AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 121 GTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG 181 AAACCAGGAAAAGCTCCTAAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC Gaps Length 19035; ö 1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGC Indels Score 387; DB 19; Pred. No. 7.1e-108; .. 0 0; Mismatches 100.0%; 387; Conservative Similarity 61 Query Match Best Local S Best Loca Matches ઠ ò g · 8 셤 8 ద

241 CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300

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RESULT 4
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                                                                                                                         CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCTG 7840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyronmetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclarotic; heparotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.
                                                                                     CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New humanized anti-Fas antibody, useful for treating or inflammatory or autoimmune disease, induces apoptosis secells with abnormal Fas-Fas ligand systems
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disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,

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multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a human immunoglobulin light chain kappa variable region subgroup type I which is used in the construction of humanised anti-Fas antibody
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light chain subunit; apoptosis; immunosuppressive; antiallergic;
autoimmune disease; allergy; atopic; FCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21; Length 729;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 729 BP; 192 A; 200 C; 182 G; 155 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           constructs described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 342.2; DB 2
Pred. No. 1.1e-94;
0; Mismatches 28
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Best Local Similarity 92.8%;
Matches 359; Conservative
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The invention relates to a preventive or treating agent for diseases caused by abnormality in Fas/Fas ligand system containing as the active component an antibody having as the light chain subunit a polypeptide containing residues 1-218 of one of 3, 239 residue amino acid sequences, or residues 1-451 of one of 3, 470 residue amino acid sequences, fully defined in the specification and having an activity of combining specifically with mammalian Fas and an activity of inducing apoptosis in a cell expressing Fas. The agent has immunosuppressive and antiallergic activity and is used for preventing and treating autoimmune diseases, allergy, atopy and others. The present sequence is that of a PCR primer, useful to the invention.
                                                                     anti-Fas antibody, used for preventing and
                                                                                                                                          Example 15 (Preparatory); Page 40; 194pp; Japanese.
                                                                                            treating autoimmune diseases, allergy, and atopy
                                                                     containing humanised
                    WPI; 2002-145113/19
                                                                  Drug
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Seguence 729 BP; 192 A; 200 C; 182 G; 155 T; 0 other;

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                                                                                                                                           61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
                                                                                                                                                                              AGATGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGA 126
                                                                                                                                                                                                                  GTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTTAAATTGGTATCAGCAG 180
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                                                                                            AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC
                                                                       1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGGTGCC
                                                                                                                                                                                                                                                                                                                           AAACCAGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC
                                   Gaps
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88.4%; Score 342.2; DB 24; Length 729;
                                   28; Indels
                Pred. No. 1.1e-94;
                                   0; Mismatches
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                92.8%;
                Best Local Similarity 92.8
Matches 359; Conservative
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Human ovarian antigen HRACW30 cDNA, SEQ ID NO:121.
          ABQ54241 standard; cDNA; 1106
                               (first entry)
                                22-AUG-2002
                     AB054241;
RESULT 5
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ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;

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Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; chromosome 2p12;
                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                         07-JUN-2001; 2001WO-US18569.
                                                                                       07-JUN-2000; 2000US-209467P.
                                                                                                                                                                               neurological diseases
                                                                                                                    Birse CE, Rosen CA;
                                                                                                                                   WPI; 2002-147878/19
                                                                                                                                         P-PSDB; ABP41164.
                                           WO200200677-A1.
                              Homo sapiens.
                                                          03-JAN-2002
                dene; ss.
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Claim 1; SEQ ID No 121; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP41054-CC ABP43228) and to cDNAs encoding them (ABO\$4131-ABQ\$6305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens and the use of ovarian antigens, and the use of ovarian antigen polynucleotides adainst human ovarian antigens, and the use of ovarian antigen polynucleotides adainst human ovarian antigens, and the use of ovarian polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, clasorders (e.g., infertility, disorders of pregnancy, anovulation, clasorders, infertility, disorders of pregnancy, anovulation, cshock syndrome, ovarian cysts, and dysmenorrhoea), and toxic cshock syndrome, inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired confined system disorders (e.g., anaemia), cardiovascular disorders (c.g., anaemia), chimiary system disorders. Ovarian antigen polypoptides and confined and confirmation of individuals and in forensic analysis, and the confirmation of individuals and in forensic analysis, and the confirmation of individuals and in forensic analysis, and the present antibodies represented the analysis and an antibodies and an antibodies and an antibodies and an antibodier and an useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents cDNA encoding a human ovarian antigen of the nvention.

printed Note: The sequence data for this patent did not form part of the printer specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 1106 BP; 321 A; 296 C; 247 G; 227 T; 15 other;

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61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
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                                                                                          1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGGTGCC
                                                                                                                                        79 Argeacareagegrecedereagerecregecrecrecracreregecreegereee
                                                Gaps
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87.6%; Score 339; DB 24; Length 1106; 90.7%; Pred. No. 1.2e-93; ive 7; Mismatches 29; Indels 0
                                                Matches' 351; Conservative
                        Local Similarity
    Query Match
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P-PSDB; AAB99115
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GTCACCATCACTTGCAGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG 180
          CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG
                                       AAACCAGGAAAAGCTCCTAAGCTCCTGATCTAGCATCCAGTTTGCAAAGTGGGGGTC
                                                                                                                        CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC
                                                                                                                                                                                                                                                                                                   Human anti-tumour antigen antibody light chain variable region cDNA
                                                                                                                                                                                                                                                                                                                      Human; tumour antigen; cancer; monoclonal; antibody; light chain; variable region; medicine; pharmacology; biochemistry; ds.
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86.4%; Score 334.2; DB 18; Length 396;
Best Local Similarity 91.5%; Pred. No. 2.4e-92;
Matches 354; Conservative 0; Mismatches 33; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a human anti-tumour antigen monoclonal antibody (MAb) light chain variable region, useful medicine, pharmacology and biochemistry. The isotype of a MAD secreted by the human/human hybridoma HT was determined to be and kappa. Human MAb was purifited, and the antigen recognised human MAb CLN"-IgM identified by western blotting.
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                                                                                                                                                                GGCCAAGGGACCAAGGTGGAAATCAAA 387
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                                                                                                                                                                                                                                                                                                                                                                        location/Qualifiers
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                                                                                                                                                                                                                                      BP.
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The present invention relates to novel human monoclonal antibodies. The antibodies can bind to human Tumour Growth Factor-beta (TGF-beta) II receptor, resulting in the inhibition of the signal transduction of human TGF-beta into cells. The antibodies can be used for the prevention and treatment of diseases associated with the production of TGF-beta, such as tissue fibrosis in the lung, liver, skin, kidney or other tissues.
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                                                                                                                                                                                                                                          241 CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
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                                                                                                                               CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC 360
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                                                                                                            GTCACCATCACTTGCAGGCAAGTCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAG
                                                             1 ATGGACATGGAGGCCCACGTTCAGCTTCTGGGCTCCTGCTACTCTGGCTCCGAGGTGCC
                                                                                                                                                                             AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC
                                             AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      onoclonal antibodies recognizing human TGF-beta II receptor for treating TGF-beta associated diseases such as tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 12; Page 103-104; 118pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                             GGCCAAGGGACCAAGGTGGAAATCAAA 387
                                                                                                                                                                                                                                                                                                                                                                                              Human coding sequence SEQ ID 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
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08-NOV-2000; 2000JP-0340216.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kamada M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-343825/36.
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useful for treati
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New human monoclonal antibody that binds to activation inducible lymphocyte immunomodulatory molecule, useful for treating rheumatoid arthritis, multiple sclerosis and inflammation
                                                                                                  Claim 45; Page 267-270; 300pp; English
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              WPI; 2002-075313/10.
P-PSDB; AAU74297.
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atherosclerosis, atopy, keloid and arthritis. The present sequence was used in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus; multiple solerosis; autoimmune thyroiditis; psoriasis; hepatitis; allergic contact-type dermatitis; chronic inflammatory dermatosis; systemic lupus erythematosus; autoimmune disorder; inflammation; ss;
                                                                                                                                                                                                                                                                                                                CCATCAAGGITCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCTG
                                                                                                              1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGGTGCC
                                                                                                                                    AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-human AILIM monoclonal antibody clone Jmab-136, light chain cDNA.
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       graft versus host reaction; immune rejection; intestinal immunity;
ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiallergic, antiuleer, neuroprotective, antithyroid, vasotropic, immunosuppressive, dermatological, antiinflammatory, hepatotropic, activation inducible lymphocyte immunomodulatory molecule, AILIM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                       ..
0
                                                               Length 438;
                                                            Score 334.2; DB 22; Length
Pred. No. 2.5e-92;
0; Mismatches 33; Indels
                                      Sequence 438 BP; 103 A; 123 C; 111 G; 101 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                  GGCCAAGGGACCAAGGTGGAAATCAAA 387
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                                                             Query Match
Best Local Similarity 91.5%;
Matches 354; Conservative
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30-MAR-2001; 2001JP-0099508
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The invention relates to a novel human antibody (I), preferably a human monoclonal antibody which binds to an activation inducible lymphocyte immunomodulatory molecule (AILIM). (I) is useful for modulating signal transduction into a cell mediated AILIM, for modulating proliferation of AILIM-expressing cells, for modulating production of a cytokine from AILIM-expressing cells, and for inducing antibody-dependent cytotoxicity against AILIM-expressing cells and/or immune cytolysis or apoptosis of AILIM-expressing cells (I) is useful for treating or apoptosis of prophylaxis of delayed type allergy. (I) is useful for treating and preventing various diseases associated with AILIM-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preventing various thereases associated with Annia decorporation and/or transduction, and for inhibiting the onset and/or advancement of the diseases. (1) is useful for suppression, prevention and/or treatment of rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis, allergic context-type dermatitis, chronic inflammatory dermatosis, systemic lupus erythematosus, insulin-dependent diabetes mellitus, psoriasis, autoimmune or allergic disorders, inflammation, graft versus host reaction, graft versus host disease, immune rejection, disorders caused by abnormal intestinal inflammation, profit of the profi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human anti-mouse antigenicity (HAMA) in a host. '7 represent anti-human AILIM monoclonal antibody coding
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Matches 351; Conservative 0; Mismatches
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P-PSDB; AAY56659, AAY56724.
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                                                                                             Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system; hyperimmunity disorder; autoimmune disease; diabetes; graft rejection; proliferative disorder; cancer; immunodeficient disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)-4 containing specified heavy and light chain sequences, useful for treating, e.g. immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes a kappa chain of an antibody of the invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)-4. Antibodies of the invention are composed of a heavy chain variable region, comprising a modified contiguous sequence from a FRI-FR3 sequence encoded by a human VH3-33 family gene. The modifications are contained in CDR1, CDR2 and/or framework regions. The antibodies may be used to inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity disorders (e.g. autoimmune disease, diabetes and graft rejection) and proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate immune system to up-regulate immunodeficient disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Davis CG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21; Length 714;
                                                                the kappa chain of immunoglobulin clone 11.2.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gilman SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 714 BP; 188 A; 199 C; 173 G; 154 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 326.2; DB 2.
Pred. No. 8.6e-90;
0; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanke JH,
                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mueller EE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Fig 22r; 157pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.3%;
90.2%;
                                                                                                                                                                                                                                                                                                                          99WO-US30895
                                                                                                                                                                                                                                                                                                                                                       98US-0113647
                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       Neveu MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-442647/38.
P-PSDB; AAY93735.
                                                                                                                                                                                                                                                                                                                                                                                     (PFIZ ) PFIZER INC. (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                            WO200037504-A2
                                                                DNA encoding
                                                                                                                                                                                                                                                                                                                          23-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                         23-DEC-1998;
                                                                                                                                                                 sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corvalan JR;
                                 03-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 349;
                                                                                                                                                                                                                                                                                          29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanson DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
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    AAA46899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
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CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibodies containing donor complementarity determining regions and non-human primate acceptor frameworks, having reduced immunogenicity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunogenicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Andeacardadecreecedereacreeredecreerecreerecreerecreered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complementarity determining region, antibody, primate, immu
Old World ape, Old World monkey, antigen-binding affinity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of chimpanzee Vkappa cDNA clone 46-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 387 BP; 94 A; 104 C; 95 G; 94 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.9%; Score 324.6; DB 21;
89.9%; Pred. No. 2.1e-89;
cive 0; Mismatches 39;
                                                                                                                                                                                                                                    GCCCAAGGGACCAAGGTGGAAATCAAA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 67-68; 123pp; English.
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coding DNA sequence

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Antiallergic; haemostatic; immunomodulator; cytostatic; antibody; human CD40; IL-12; LPS; lipopolysaccharide; IFNgamma; interferon gamma; dendritic cell; high G28-5; CD95 expression; high G28-5; B cell line;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunoactivator, anti-tumour agent, immunosuppressant, allergy, autoimmune disease, coagulation factor VIII inhibitor, anti-CD40; gene,
for autoimmune diseases, allergy or coagulation factor VIII inhibitors syndrome. This polynucleotide sequence represents a coding DNA sequence relating to the anti-CD40 monoclonal antibody of the invention.
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                                                                                                                                                                                                                                                                               61 AGATGTGACATCCAGATGACCCAGTCTCCCATCTTCCCTGTCTGCATCTGGGGGACAGA
                                                                                                                                                                                                                                                                                                   GTCACCATCACTTGCAGGCCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                   AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAACCAGGAAAGCTCCTAAGCTCCTGATCTATGATGCCTCCAATTTGGAAAGTGGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ccarcaaggricagggaggagagarcrggacagarrrcacrcaccarcaggagggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGCCTGAAGATTTTGCAACTTATTACTGTCAACAGTTTAATAGTTACCC---GACGTTC
                                                                                                                                                                                                 ATGGACATGAGGGTCCCCGGTCAGCTCCTGGGCTCCTTCTGCTCTGGCTCCCAGGTGCC
                                                                                                                    DB 25; Length
                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-CD40 monoclonal antibody related DNA SEQ ID No 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takahashi
                                                                             Sequence 448 BP; 111 A; 123 C; 114 G; 100 T; 0 other;
                                                                                                                                                             29;
                                                                                                                                        .2e-89;
                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen X,
                                                                                                                    324.6;
No. 2.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCCAAGGGACCAAGGTGGAAATCAAA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   442
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                                                                                                                      Score
                                                                                                                                        Pred.
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2001JP-0142482.
2001JP-0310535.
                                                                                                                  Query Match 83.9%;
Best Local Similarity 91.7%;
Matches 355; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yoshida H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ğ
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11-MAY-2001; 2
05-OCT-2001; 2
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                                                                                                                                                                                                                                          59
                                                                                                                                                                                                                                                                                                                      119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an antibody to human CD40, or its functional fragment, has at least one of the following properties: acting on dendritic cells to produce IL-12 in the presence of LB9 (lipopolysaccharide) and IFNgamma (interferon gamma); acting on dendritic cells to activate maturity of the dendritic cells with high G28-5 antibody, and activating CD95 expression with high G28-5 antibody against B cell line. Such antibodies or functional fragments can be used as immunoactivators, anti-tumour agents, immunosuppressants, and as remedies
                                                                                                   240
                                                                                                                                        240
                                                                                                                                                                                 300
                                                                                                                                                                                                                                                                                   CAACCTGAAGATTTTGCAACTTATTACTGTCAGGATGGTTACGGTACACCACTTTC 360
                        GTCACCATCACTTGCAGGCAAGTCAGGACATTAGGTATTATTTTAAATTGGTATCAGCAG 180
                                                           Grcaccarcacrreceegeaagrcagagcarragcaacrarragagrregrarcagcag 180
                                                                                                                                                                                                                        CCATCAAGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antiallergic; haemostatic; immunomodulator; cytostatic; antibody; human CD40; IL-12; LP8; lipopolysaccharide; IPRgamma; interferon gamma; dendritic cell; high G28-5; CD5 expression; high G28-5; B cell line; immunoactivator; anti-tumour agent; immunosuppressant; allergy; autoimmune disease; coagulation factor VIII inhibitor; anti-CD40; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD40,
                                                                                                                                                                               CCATCAAGGITCAGCGCCAGTGGATCTGGGACAGGTTCACTCTCACCGTCAGCAGCCTG
                                                                                                                                                                                                                                                              CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC
                                                                                                                                        AAACCAGGGAAAGCCCCTAAGCTCCTGATCTATTATGCATCCACTTTGCAAAGTGGGGTC
                                                                                                   AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-CD40 monoclonal antibody with antagonist/agonist activity to CD40 or functional fragment, is useful in the treatment of e.g. autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-CD40 monoclonal antibody related DNA SEQ ID No 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen X,
                                                                                                                                                                                                                                                                                                                                          387
                                                                                                                                                                                                                                                                                                                                                                                 GGTGGAGGACCAAGGTGGAGATCAAA 387
                                                                                                                                                                                                                                                                                                                                        GGCCAAGGGACCAAGGTGGAAATCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 26; Page 52-53; 94pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Force
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11-MAY-2001; 2001JP-0142482.
05-OCT-2001; 2001JP-0310535.
26-OCT-2001; 2001US-0040244.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KIRI ) KIRIN BEER KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2003-120463/11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-120463/
P-PSDB; ABJ36932.
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CCATCAAGGTTCAGCGGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AGATGTGACATCCAGATGACCCAGTCTCCTTCTTCCTTGTCTGCATCTGTAGGAGACAGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCACCATCACTTGCAGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides an antibody (Ab) comprising donor CDRs (complementarity determining regions) derived from a non-human antigenspecific donor antibody, and an acceptor framework from a non-human primate. The Abs are prepared by grafting CDRs from a non-human antigenspecific donor antibody onto homologous Old World ape or monkey acceptor frameworks. The Abs have reduced immunogenicity and are better tolerated in humans (because of the close similarity between the human and primate proteins), but retain the full antigen-binding affinity of the donor
                                                                                                                                                                                                                                                                                                                  Antibodies containing donor complementarity determining regions and non-human primate acceptor frameworks, having reduced immunogenicity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 AAACCGGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCACTTTCCAAAGTGGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunoglobulin light chain variable region partial transcript.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
83.0%; Score 321.4; DB 21;
Best Local Similarity 89.4%; Pred. No. 2e-88;
Matches 346; Conservative 0; Mismatches 41; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 390 BP; 91 A; 111 C; 96 G; 92 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCCAAGGGACCAAGGTGGAAATCAAA 387
                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Page 96-97; 123pp; English
                                                                                                                                                 SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                    99WO-US09131.
                                                                                                 98US-0083367
                                                                                                                                                                                                                                              WPI; 2000-023265/02.
P-PSDB; AAY56672, AAY56737.
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                                                  28-APR-1999;
                                                                                                    28-APR-1998;
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04-NOV-1999
                                                                                                                                                                                                   raylor AH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                              fragment, has at least one of the following properties: acting on dendritic cells to produce IL-12 in the presence of LPS (lipopolygaccharide) and IFNgamma (interferon gamma); acting on dendritic cells to activate maturity of the dendritic cells with high G28-5 antibody; and activating CD95 expression with high G28-5 antibody against a cell line. Such antibodies or functional fragments can be used as immunoactivators, anti-tumour agents, immunosuppressants, and as remedies for autoimmune diseases, allergy or coagulation factor VIII inhibitors syndrome. This polymucleotide sequence represents a coding DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCACCATCACTTGTCGGGGGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAG 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAACCAGGAAAAGCTCCTAAGCTCCTGATCTAGTTGCATCCAGTTTGCAAAGTGGGGTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGGATCCAGTTTGCAAAGTGGGGTC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAGCAGTTTCCCTCGGACATTC 418
                                                                             CD40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunogenicity;
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                                                                             Anti-CD40 monoclonal antibody with antagonist/agonist activity to CD40 or functional fragment, is useful in the treatment of e.g. autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGCCTCCTTCTGCTCTGGCTCCCAGGTGCC
                                                                                                                                                                                                                          The invention relates to an antibody to human CD40, or its functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         relating to the anti-CD40 monoclonal antibody of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complementarity determining region; antibody; primate; immunos 
Old World ape; Old World monkey; antigen-binding affinity; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

83.5%; Score 323; DB 25; Length 728;
Best Local Similarity 89.7%; Pred. No. 8.3e-89;
Matches 347; Conservative 0; Mismatches 40; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequence of Cynomologous Vkappa cDNA clone 4-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 728 BP; 183 A; 201 C; 195 G; 149 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCCAAGGGACCAAGGTGGAGATCAAA 445
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                                                                                                                                                                             Claim 16; Page 59-60; 94pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ39340 standard; DNA; 390
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       WPI; 2003-120463/11
P-PSDB; ABJ36940.
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Length 390; Indels 120

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A novel composition has been developed which comprises an immunoglobulin (Ig) having an affinity constant (Ka) of at least 2 multiply 1000000000 M-1 for binding to a predetermined human antigen. The present sequence represents a human light chain variable region partial nuclectide sequence, 10CS kappa, which encodes an amino acid sequence from a claimed immunoglobulin that specifically binds human CD4. The anti-CD4 antibodies may be used in therapeutic and diagnostic applications, especially for the treatment of human diseases. These autoimmune reactions, inflammatory response and transplant rejection. Transgenic animals are capable of producing heterologous antibodies of funditible isotypes by undergoing isotype switching. These animals produce a first Ig type that is necessary for antigen-stimulated B-cell maturation and can switch to encode and produce one or more subsequent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
              affinity constant; human; antigen; hybridoma; B cell; transgene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.2%; Score 318.2; DB 18; Length 388; 88.9%; Pred, No. 1.9e-87;
                             transgenic, mouse, CD4, antibody, autoimmune, inflammatory, transplant rejection; 88.
                                                                                                                                                                                                                                                                                                                                                                        Novel anti-CD4 antibody produced by transgenic mice - used treatment of auto-immune disease etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 388 BP; 89 A; 107 C; 97 G; 95 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 44; Page 255; 396pp; English.
                                                                                                                                                                                          96WO-US16433.
                                                                                                                                                                                                                                95US-0544404.
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                                                                                                                                                                                                                                                                 (GENP-) GENPHARM INT INC
                                                                                                                                                                                                                                                                                                                                        WPI; 1997-235888/21
                                                                                                                                                                                                                                                                                                     Lonberg N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                            10-OCT-1996;
                                                                                                                                                                                                                                10-OCT-1995;
                                                                                     Homo sapiens
                                                                                                                       409713852-A1
                                                                                                                                                          17-APR-1997.
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                                                                                                                                                                                                                                                                                                     Kay RM,
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AAV39232-41 represent functional transcripts of a human IgGKappa anti-CD4 antibody. The sequences are isolated from 5 different transgenic mouses hybridoma cell lines. The specification describes transgenic monse hybridoma cell lines. The specification describes transgenic mon-human animals, especially a mouse, which are capable of producing a human heterologous antibodies of multiple isotypes by undergoing isotype switching. The transgence animals have human heavy and light chain transgenes. The transgenes are capable of functionally rearranging a heterologous diversity (D) gene in a heavy Chain transgene comprising at least one V, D and J gene segment, and one constant region gene segment. The immunoglobulin (Ig) light chain constant region gene segment in the gene segment and one constant region gene segment are heterologous to the transgenic animal. The antibody can be used to prevent efflux of neutrophils from cantibodies are used to reduce undesirable autoimmune reactions, inflammatory responses and rejection of transplanted organs. The antibodies can reduce tissue damage and prolong survival in animal models of acute adult respiratory distress syndrome (ARDS) and cid induced lung injury. The antibodies can also be used for the treatment of vasculitis, septic shock, allergic reactions (e.g.
                                                                                                                                                                                                                                                                                       CD4 binding;
                                                                                                                                                                                                                                                               Transgenic animal; human heterologous antibody; transgene; isotype switching; neutrophil efflux; reperfusion injury; CD4 binding autofimmune reaction; inflammatory response; transplant rejection; acid induced lung injury; acute adult respiratory distress syndrome; ARDS; vasculitis; septic shock; allergic reaction; asthma;
                                                                                                                                                                                                                               Functional Kappa transcript isolated from transgenic cell line 10C5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hybridoma producing antibody specific for interleukin-8 -
prevent efflux of neutrophils from vasculature, and treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 388 BP; 89 A; 107 C; 97 G; 95 T; 0 other;
361 GGCCAGGGACCAAGCTGGAGATCAAA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 41; Page 304; 452pp; English.
                                                                                                                  BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0758417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             asthma) and cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-US21803.
                                                                                                                  AAV39239 standard; DNA; 388
                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENP-) GENPHARM INT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-333306/29
                                                                                                                                                                                                                                                                                                                                                                      cystic fibrosis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kay RM, Lonberg N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reperfusion injury
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1997;
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                                                                                                                                                                                            18-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                        AAV39239;
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                                                                               RESULT 15
                                                                                                   AAV39239
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Gaps

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82.2%; Score 318.2; DB 19; Length 388; 88.9%; Pred. No. 1.9e-87; ive 0; Mismatches 43; Indels 0;

Best Local Similarity 88.9 Matches 344; Conservative

361 GGCCAAGGGACCAAGGTGGAAATCAAA 387

Query Match

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241 CCATCAAGGTTCAGCGGCAGTGGATCTCGGCACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
                                                                                                                                       241 CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG 300
1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGCTCCTTCTGCTCTGGCTCCCAGGTGCC 60
       1 AIGGACATGATGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTCTGGTTCCCAGGTTCC 60
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Search completed: December 29, 2003, 16:25:38 Job time : 169.851 secs

Sequence 25, Appl Sequence 10, Appl Sequence 16, Appl Sequence 26, Appl Sequence 1811, Ap Sequence 1811, Ap Sequence 1811, Ap Sequence 37859, A

Sequence 56, Appl Sequence 1210, Ap Sequence 1210, Ap Sequence 1210, Ap

Sequence 7

Sequence 11,

Sequence 8365, Appl Sequence 56, Appl Sequence 22, Appl Sequence 5, Appli Sequence 53, Appl Sequence 81, Appl Sequence 24, Appl

Sequence 2039, Ap Sequence 2039, Ap Sequence 2039, Ap Sequence 79, Appl Sequence 19, Appl

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APPLICANT: REFF, Mitchell E.
KLOSTZER, William S.
NAKAMURA, TAKENİKO
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
ANTIBODIES AND USE THEREOF AS THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version #1.30
5 US-10-040-244-11

5 US-10-158-646-55

US-10-158-646-56

0 US-10-158-646-56

0 US-10-158-646-56

0 US-10-168-1210

4 US-10-046-925-1210

0 US-09-19-344-7

US-09-919-344-7

US-09-910-389-221-10

US-09-910-389-221-10

US-09-910-389-221-10

US-09-910-389-231-10

US-09-910-389-385-1811

4 US-10-46-935-1811

5 US-10-146-935-1811

5 US-10-168-646-65

10S-09-910-238-1811

US-09-910-238-1811

US-09-910-238-1811

US-09-910-238-1811

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US-09-910-238-1811

US-09-910-238-1811

US-09-910-243-56

US-09-910-243-53

US-09-910-243-53

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US-09-910-243-53
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US-10-146-502-2039
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US-09-905-243-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EMP PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PSTEMIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,441
FILING DATE: OS-Feb-1998
CLASSIFICATION: AUNROWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/803,085
FILING DATE: 20-FEB-1997
ATTORNEX/AGENT INPORMATION:
NAME: TESKIA. ROBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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Publication No. US20030086921A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703) 836
INFORMATION FOR SEQ ID NO: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Alexandria
STATE: Virginia
     JS-09-019-441-3
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305.8
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         Sequence 3, April Sequence 125, App Sequence 125, App Sequence 29, App Sequence 27, App Sequence 27, App Sequence 15, App Sequence 57, App Sequence 15, App Sequence 186, App Sequence 13, App Sequence 11, Appl Sequence 11, Appl
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2371.523 Million cell updates/sec
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                                                                                                                                        ; Search time 559.115 Seconds
                                                                                                                                                                                                                                                    1 ATGGACATGAGGGTCCCCGC......GGACCAAGGTGGAAATCAAA 387
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*

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                           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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1 US-10-103-686-3

3 US-10-316-849-31-125

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1 US-09-95-243-27

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US-09-844-684-13
US-10-040-244-13
US-09-844-684-11
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                                                                                                                                        December 29, 2003, 19:01:43
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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321.4 321.4 321.4 321.4 311.4

Score

Result Š.

Post-processing:

Database

Scoring table:

Searched:

Perfect score:

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Sequence:

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Publication No. US20030059424A1
GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
NAKAWURA, Takehiko
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
ANTIBODIES AND USE THEREOF AS THERAPEUTICS
                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                              100.0%; Score 387; DB 11; Length 387; 100.0%; Pred. No. 6e-114; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/103,686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCCAAGGGACCAAGGTGGAAATCAAA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 GGCCAAGGGACCAAGGTGGAAATCAAA 387
                                                                                                                                                                       LOCATION: 67..387
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
            LENGTH: 387 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                    NAME/KEY: mat peptide LOCATION: 67..387
SEQUENCE CHARACTERISTICS:
                                                                                                                        1..387
                                                                                                                                                                                                                                                             Matches 387; Conservative
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                                                                                                          NAME/KEY:
                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                Similarity
                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-103-686-3
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Best Local
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61 AGATGTGACATCCAGATGACCCAGTCTCCCATCTTCCCTGTCTGCATCTGTAGGGACAGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 387; DB 15;
100.0%; Pred. No. 6e-114;
tive 0; Mismatches 0;
                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Serizawa, No. US20030170817Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Haruyama, Kaori
APPLICANT: Tamaki, İkuko
APPLICANT: Tamaki, İkuko
APPLICANT: Takahashi, Tohru
TILE OF INVENTION: Anti-Fas Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCCAAGGGACCAAGGTGGAAATCAAA 387
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                LENGTH: 387 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.0
Matches 387; Conservative
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LENGTH:

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GENERAL INCREMINON:
APPLICANT: Teuji, Takashi
APPLICANT: Teuji, Takashi
APPLICANT: Teuji, Takashi
APPLICANT: Teuji, Wasunari
APPLICANT: Hori, No. US20020102658Aluaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: HUMAN MONOCLONAL TRANSDUCTION MOLECULE ALLIM AND
TITLE OF INVENTION: HPARMACEUTICAL USE THEREOF
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
TITLE OF TARENT APPLICATION NUMBER: US/09/859,053
CURRENT APPLICATION NUMBER: US 2001-99508
PRIOR APPLICATION NUMBER: UP 2001-19508
PRIOR APPLICATION NUMBER: UP 2000-147116
PRIOR APPLICATION NUMBER: UP 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                  187 AAACCAGGGAAAGCCCCTAAGCTCCTGATÇTATGCTGCATTCTGCAAATGCGGGTC 246
                                                                                                                                                                                                                                                                                                                                                                                                  CCATCAAGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGGAGTCTG 306
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                                                                                                                      AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
                                                                                                                                              GTCACCATCACTTGCAGGCCAAGTCAGGACATTAGGTATTATTTTAAATTGGTATCAGCAG 180
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Indels
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28;
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Pred. No. 2.6e-
0; Mismatches
Mismatches
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Patent No. US20020102658A1
GENERAL INFORMATION:
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ilarity 90.7%;
Conservative (
Matches 359; Conservative
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LOCATION: (39) ... (104)
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: 3'UTR
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Best Local Similarity
Matches 351; Conserv
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NAME/KEY:
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NAME/KEY:
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                                PRIOR APPLICATION NUMBER: US/09/499, 662
PRIOR FILING DATE: 2000-02-09
PRIOR PLING DATE: SARLIER APPLICATION NUMBER: US 09/053,583
PRIOR PLING DATE: EARLIER FILING DATE: 1998-04-01
SEQ ID NO 125
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                                                                                                                                                                                                                                                                       Length 729;
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                                                                                                                                                                                                                                                                     Score 342.2; DB 13; Length
Pred. No. 1.8e-99;
0; Mismatches 28; Indels
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Pred. No. 1.8e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Serizawa, No. US20030103976Alufusa
APPLICANT: Serizawa, No. US20030103976Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Tamaki, Ikwo
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
IENGTH: 729
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CURRENT APPLICATION NUMBER: US/10/384,933
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92.8%;
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 92.8%;
Matches 359; Conservative
                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-216-484-125
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Best Local Similarity
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241 CCATCAAGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 CAACCTGAAGATTTTGCAACTTATTACTGTCAGCATGGTTACGGTACACATCCCACTTTC 360
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Sequence 15, Application US/09844684
Sequence 15, Application US/09844684
PSequence 15, Application US/0984684
Sequence 15, Application Sequence 15, Application Sequence 15, Applicant: Gemini Science, INC.
Applicant: La Jolla Institute For Allergy and Immunology
TITLE OF INVENTION: HUMAN ANTI-CD40 ANTIBODIES AND METHODS OF MAKING SAME
FILE REPERENCE: 21286/0276339
CURRENT APPLICATION NUMBER: US/09/844,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GTCACCATCACTTGCCGGGCAAGTCAGAGCATTAGCAACTATTTGAGTTGGTATCAGCAG
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                                                                                                                                            Sequence 27, Application US/09905243

Patent No. US200200620091

GENERAL INFORMATION:

APPLICANT: Taylor, Alexander H

TITLE OF INVENTION: Monoclonal Antibodies with Reduced

TITLE OF INVENTION: Immunogenicity

FILE REPERENCE: P50770

CURRENT APPLICATION NUMBER: US/09/905,243

CURRENT PILING DATE: 2001-07-16

PRIOR FILING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 97

SOFTWARE: Fast SEQ for Windows Version 3.0

FENCINE TO NOS: 97

SOFTWARE: Fast SEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 324.6; DB 9;
Pred. No. 6.5e-94;
0; Mismatches 39;
387
                          361 GGCCCTGGGACCAAAGTGGAAATCAAA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 GGCCAAGGGACCAAGGTGGAAATCAAA 387
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GGCCAAGGACCAAGGTGGAAATCAAA
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89.9%;
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Matches 348; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , NAME/KEY: CDS
; LOCATION: (1)...(387)
US-09-905-243-27
                                                                                                                                         -09-905-243-27
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361
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Publication No. US20030086930A1;
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES;
FILE REFERRICE: PC23019A;
CURRENT FILING DATE: 2002-05-22;
PRIOR APPLICATION NUMBER: 60/293042;
PRIOR APPLICATION NUMBER: 60/293042;
PRIOR FILING DATE: 2001-05-23;
NUMBER OF SEQ 1D NOS: 39;
SOFTWARE: Patentin Ver. 2.1
SEQ 1D NO 18
LENGTH: 74
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llarity 90.2%; Pred. No. 2.5e-94;
Conservative 0; Mismatches 38;
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US-10-153-382-18
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US-10-153-382-18
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Pred. No. 6.9e-93;
0; Mismatches 41;
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Patent No. US20020062009A1
GENERAL INFORMATION:
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Best Local Similarity 89.4%;
Matches 346; Conservative (
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; FEATURE:
; NAMMY/KEY: CDS
; LOCATION: (1)...(390)
US-09-905-243-57
      Matches 347; Conservative
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APPLICANT: KIRIN BEER KABUSHIKI KAISHA
APPLICANT: FONCE, WALKER F.
APPLICANT: TAKHASHI, NOBUAKI
APPLICANT: TAKHASHI, NOBUAKI
APPLICANT: TAKHASHI, NOBUAKI
APPLICANT: TAKHASHI, NOBUAKI
TILE OF INVENTION: ISOLANDATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTIBOD
FILE REFERENCE: 021286/0272501
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 05/20,601
PRIOR PILING DATE: 2001-427
PRIOR PILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATCHIN VEY: 3.0
SEQ ID NO 15
LENGTH: 728
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                                                                                                                                                                                                                                                                                                                                                        Length 728;
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                                                                                                                                                                                                                                                                                                                                                        83.5%; Score 323; DB 10;
89.7%; Pred. No. 2.7e-93;
ive 0; Mismatches 40;
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CURRENT FILING DATE: 2001-04-27
PRIOR PAPLICATION NUMBER: US 60/200,601
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 15
SSPTWARE: PREENTIN VEr. 2.1
SEQ ID NO 15
LENGTH: 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/10040244
Publication No. US20030059427A1
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89.7%;
                                                                                                                                                                                                                                                                                                                                                        Query Match 83.5
Best Local Similarity 89.7
Matches 347; Conservative
                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-844-684-15
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ORGANISM: Homo sapiens
US-10-040-244-15
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Best Local Similarity
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                                                                                                                                                                                                                                                                                       APPLICANT: Secriet, Teacher APPLICANT: Secriet, Darrick APPLICANT: Earter, Darrick APPLICANT: Famer Gary R. APPLICANT: Fames Gary R. APPLICANT: Fames Garole L. APPLICANT: Smith, Carole L. APPLICANT: Scolk, John A Margarita APPLICANT: Scolk, John A Margarita STILE OF INVENTION: AND DIAGNOSIS OF COLON CANCER TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER TITLE OF INVENTION NUMBER 12/12/1.563 CURRENT PILICATION NUMBER 12/12/1.563 CURRENT FILING DATE: 2002-01.31 NUMBER OF SEQ ID NOS: 3417 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

83.0%; Score 321.4; DB 15; Length 537;
Best Local Similarity 89.4%; Pred. No. 7.8e-93;
Matches 346; Conservative 0; Mismatches 41; Indel8 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCCAAGGACCAAGGTGGAAATCAAA 387
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372 GGCCAAGGACCAAGGTGGACATCAAA 398
                                                                                                                         Sequence 186, Application US/10066543 Publication No. US20030087818A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
US-09-844-684-13
; Sequence 13, Application US/09844684
                                                                                                                                                                                     APPLICANT: Jiang, Yuqiu
APPLICANT: Pyle, Ruth A.
APPLICANT: Xu, Jiangchun
APPLICANT: Indirias, Carol Yoseph
APPLICANT: Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: n = A,T,C or US-10-066-543-186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                          JS-10-066-543-186/c
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                                                                                     301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC 360
                                                                                                                                                         181 AAACCGGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCACTTTCCAAAGTGGGGTC 240
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APPLICANT: Ludirias, Carol Yoseph
APPLICANT: Indirias, Carol Yoseph
APPLICANT: Lodges, Michael J.
APPLICANT: Secriet, Heather
APPLICANT: Carter, Darrick
APPLICANT: Garter, Darrick
APPLICANT: Smith, Carole L.
APPLICANT: Suith, John Mergarita
APPLICANT: Stolk, John Mergarita
APPLICANT: Stolk, John Mergarita
APPLICANT: Stolk, John Mergarita
APPLICANT: Margarita
APPLICANT: Stolk, John Mergarita
FILE REFERENCE: 210121.563
CURRENT APPLICATION NUMBER: US/10/066,543
CURRENT APPLICANTON NUMBER: 2002-01-31
NUMBER OF SEQ ID NOS: 3417
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 2025
LENGTH: 514
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Pred. No. 7.7e-93;
0; Mismatches 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 89.4%;
Matches 346; Conservative
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APPLICANT: Pyle, Ruth A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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US-10-066-543-2025
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Sequence 11, Application US/09844684

Parent No. US20020142358A1

GENERAL INFORMATION:
PAPLICANT GEMINI SCIENCE, INC.
APPLICANT: LA JOLLA INSTITUTE FOR ALLERGY AND IMMUNOLOGY
TITLE OF INVENTION: HUMAN ANTI-CD40 ANTIBODIES AND METHODS OF MAKING SAME
FILE REFERENCE: 21286/0276339
CURRENT APPLICATION NUMBER: US/09/844,684

CURRENT PILING DATE: 2001-04-27

PRIOR APPLICATION NUMBER: US 60/200,601

PRIOR PILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 11

SEQ ID NO 11

LENGTH: 698
                                                                                                                                                                                                                                                                                                                                              181 AAACCAGGAAAAGCTCCTAAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC 240
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                                                                                                                              Score 321.4; DB 15; Length 716;
Pred. No. 8.7e-93;
0; Mismatches 41; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 698;
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Pred. No. 1e-89;
0; Mismatches 47; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 GGCCAAGGGACCAAGGTGGAAATCAAA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCCAAGGGACCAAGGTGGAGATCAAA 433
                                                                                                                                83.0%;
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Best Local Similarity 87.9%;
Matches 340; Conservative
                                                                                                                              Query Match
Best Local Similarity 89.4
Matches 346; Conservative
                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-244-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-844-684-11
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                     LENGTH: 716
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Sequence 13, Application US/10040244
Publication No. US20030059427A1
GENERAL INFORMATION:
APPLICANT: KIRIN BEER KABUSHIKI KAISHA
APPLICANT: FORCE, WALKER F.
APPLICANT: MIKAYAMA, TOSHFUMI
TITLE OF INVENITON: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTIBOD
FILE REFERENCE: 021286/0272501
TITLE OF INVENITON: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTIBOD
FILE REFERENCE: 021286/0272501
CURRENT APPLICATION NUMBER: US/10/040,244
CURRENT PILING DATE: 2000-4-28
PRIOR FILING DATE: 2000-4-28
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
SPRIOR FILING DATE: 2001-04-27
SOFTWARE: PATCHIN VORTE: 2010-04-27
SOFTWARE: PATCHIN VORTE: 2010-04-27
SOFTWARE: PATCHIN VORTE: 2010-04-27
SOFTWARE: PATCHIN VORTE: 3.0
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GEMINI SCIENCE, INC.
APPLICANT: LA JOLLA INSTITUTE FOR ALLERGY AND IMMUNOLOGY
TITLE OF INVENTION: HUMAN MATI-CD40 ANTIBODIES AND METHODS OF MAKING SAME
FILE REFERENCE: 21286/0276339
CURRENT APPLICATION NUMBER: US/09/844,684
CURRENT FILING DATE: 2000-04-28
FILOR APPLICATION NUMBER: US 60/200,601
FRIOR PILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTGTGTTCCCAGGTTCC 106
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89.4%; Pred. No. 8.7e-93;
ive 0; Mismatches 41; )
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Best Local Similarity 89.4
Matches 346; Conservative
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US-10-040-244-13
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Search completed: December 30, 2003, 03:42:14 Job time : 563.115 secs

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Scoring table:

Searched:

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PAPELICANT: NEFF, Mitchell E.
APPLICANT: REFF, Mitchell E.
APPLICANT: REFF, Mitchell E.
APPLICANT: REFF, Mitchell E.
APPLICANT: MACAMURA, Takehiko
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSER: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX. 1404
CITY: Alexandria
STRATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER: IBM PC compatible
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                                                                   US-09-335-697B-18
US-09-335-697B-18
US-09-740-002-18
US-09-740-002-18
US-09-620-405B-187
US-09-339-338-187
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US-09-604-287A-187
US-09-240-274-102
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US-09-240-274-221
US-09-240-274-222
US-08-836-561-70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Teskin, Robin L.
REGISTATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08803085 Patent No. 6011138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 1..387
FEATURE:
                         ; NAME/KEY:
; LOCATION:
US-08-803-085-3
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206, App
4, Appli
1, Appli
                                                                                                                                                       December 29, 2003, 16:08:50 ; Search time 42.5992 Seconds (without alignments) 4009.823 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                        1 ATGGACATGAGGGTCCCCGC......GGACCAAGGTGGAAATCAAA 387
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-08-157-101A-4
US-08-157-101A-4
US-09-042-35-360
US-09-042-35-360
US-08-434-224-16
US-08-634-224-16
US-08-634-224-16
US-08-634-224-16
US-08-634-224-16
US-08-635-878-16
US-08-970-057-16
US-09-35-697B-16
US-09-35-393-393
US-09-042-35-393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              569978 seqs, 220691566 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                          OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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318.2 318.2 316.6 308.6 307

Result

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GTCACCATCACTTGCAGGCCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG 180
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
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APPLICATION NUMBER: US 06
FILING DATE: 22-JUL-1993
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COMPUTER READABLE FORM:
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APPLICANT: BARNET, RICHARD S.
APPLICANT: BARNET, RICHARD S.
APPLICANT: BARNET, RICHARD S.
TITLE OF INVENTION: MAMMALIAN CELLS VIA HOMOLOGOUG RECOMBINATION AND TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME
TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME
TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME
FILE REPERENCE: 037003-0275807
CURRENT PELLING DATE: 1999-06-30
FRIOR FILING DATE: 1999-06-30
PRIOR PELLING DATE: 1999-02-13
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PACENTIN VECTOR S.
SEQ ID NO 3
LINGTHING DATE: 1997-03-14
SEQ ID NO 3
LINGTHING DATE: 1997-03-14
SEQ ID NO 3
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US-09-343-485A-3
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100.0%; Pred. No. 4.2e-112;
iive 0; Mismatches 0;
      100.0%; Pred. No. 8.8e-113; ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 387; Conservative
                           Matches 387; Conservative
        Similarity
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US-09-042-353-358
Sequence 358, Application US/09042353
Sequence 358, Application US/09042353
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
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MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-UUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 26-APR-1993
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Sequence 206, Application US/08758417A
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Best Local Similarity 88.9
Matches 344; Conservative
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FILING DATE: 10-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 0-0-DC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: APPLICATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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88.9%; Pred. No. 4.6
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                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 88.9
Matches 344; Conservative
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RESULT 4 US-08-758-417A-206

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                                              Transgenic No. 6300129-Human Animals for Producing Heterologous Antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.2%; Score 318.2; DB 4
88.9%; Pred. No. 4.6e-91;
live 0; Mismatches 43
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APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/758,417A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILLING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
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APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/728,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DESCRIPTION: SEQ ID NO: 206:
                                                                                                                                                                                                                                                                     ZIP: 94111-3834
COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
APPLICANT: Lonberg, Nils
Kay, Robert M.
TITLE OF INVENTION: Transgenic No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Serafini, Andrew T. REGISTRATION NUMBER: 41,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 02-Dec-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                    CITY: San Francisco
STATE: California
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61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
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33 ATGGACATGAGGGTCCCCGCTCTGGGGCTCCTGCTGCTCTCTGGTTCCCAGGTGCC 92
                                                                                                                                                                                                                                    GTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG
                                                                                                                                                                                                                                                                                                                                                                 181 AAACCAGGAAAAGCTCCTAAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC
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ATTORNEY/AGENT INFORMATION:
NAME: Smith, Willaim M
REGISTRATION NUMBER: 30,223
TELECOMMUNICATION INFORMATION:
TELEFRONE: (415) 326-2420
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08217918
Patent No. 5506132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 387 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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APPLICANT: KURIHARA, TATSUYA
APPLICANT: KURIHARA, TATSUYA
APPLICANT: TSURUCRA, SHIGERAZU
APPLICANT: TSURUCRA, NOBUO
APPLICANT: ARIMA, KENJI
APPLICANT: ARIMA, KENJI
TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
TITLE OF INVENTION: PLASMIDS THEREFOR
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 1066;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/157,101A
FILING DATE: 05-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .2e-90;
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Pred. No. 2.2e-
0; Mismatches
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08157101A
Patent No. 5808032
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NAME: TITUGS, MARLANA K
REGISTRATION NUMBER: 35843
REFERENCE/DOCKET NUMBER: 943'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3711
TELEPHONE: 202-822-0944
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88.6%;
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 88.6
Matches 343; Conservative
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STRANDEDNESS: single
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: D.C.
COUNTRY: US
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                                                                                                               121
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213 AAACCAGGGAAAGTCCCTAAGCGCCTGATCTATGCTCCAGTTTGCAAAGTGGGGTC 272
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,918
FILING DATE: 24-MAR-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: LAKE, PHILIP
APPLICANT: OSTBERG, LAKS
TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION:
US-08-217-918-1
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1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGGTGCC 60

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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 360:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 22-UUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Apple, Randolph T. REGISTRATION NUMBER: 36,
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Matches 337; Conservative
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US-09-042-351-360
Squence 360, Application US/09042353
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Squence 360, Application US/090423333
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       Length 387;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE: 17-DEC-1991
   Score 308.6; DB 1;
Pred. No. 4.9e-88;
0; Mismatches 49;
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PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/904,068
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
PILING DATE: 16-DEC-1902
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       79.7%;
87.3%;
                                        Best Local Similarity 87.3
Matches 338; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16471
                                                                                                                              PRIOR DATE:
PRIOR DATE:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
                                                                                                                                                                                                                                                                                                                 FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544 APPLICATION NUMBER: US 08/544 APPLING DATE:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
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Roland Anthony
NEUTRALIZING HIGH AFFINITY HUMAN
MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
                                                                                                                                                                                                                                                                                CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
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                                             Length 439;
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ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOSPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,376
APPLICATION NUMBER: US/08/488,376
                                                                                                                                            1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTT
                                          Score 307; DB 4;
Pred. No. 1.7e-87;
0; Mismatches 50
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FILING DATE: 07-UN-1995
CLASSIFICATION: 424
ATTORIEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: PAN, Li-Zhen
APPLICANT: WALSH, Edward E.
APPLICANT: HEARD, Cheryl Janne
APPLICANT: NEWMAN, Roland Anthony
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REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012
TELECOMMUNICATION INFORMATION:
                                             79.3%;
87.1%;
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: United States
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ADDRESSEE: Burns, Do
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                                                                   Best Local Similarity
Matches 337; Conserv
US-08-758-417A-208
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                                                  CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC 360
                                                                                               301 cagccrgaagarrrrgcaacrrarracrgccaacagrargaragraacrcgracacrrrr 360
241 CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG 300
                                                                                                                                                                                                                                                                                                                                                                                                              Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend and Crew LL
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/32,322
FILING DATE: 09-MEX-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MEX-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 22-UUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 16-DEC-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 16-DEC-1992
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APPLICATION NUMBER: US/08/758,417A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 208:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94111-3834
UTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                 GGCCAGGGACCAAGCTGGAGATCAAA 387
                                                                                                                                                 GGCCAAGGGACCAAGGTGGAAATCAAA 387
                                                                                                                                                                                                                                                                                                                 Sequence 208, Application US/08758417A Patent No. 6300129 GENERAL INFORMATION:
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: California
                                                                                                                                                                                                                                                                                          .08-758-417A-208
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Sequence 16, Application US/08634224
Patent No. 5866125
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: PAN, Li-Zhen
APPLICANT: WEARD, Cheryl Janne
APPLICANT: NEWMAN, Roland Anthony
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: MCNOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
TITLE OF INVENTION: MCNOCLONAL ANTIBODIES SPECIFIC USE THEREOF
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGAGTCACC 126
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87.4%; Pred. No. 1.5e-86;
tive 0; Mismatches 48
                                                                                                                                                     NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-2021
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
US/08/634,223
                                                                                       US/08/488,376
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                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DUMBER: US/08
FILING DATE: 07-UNN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                            : 705 base pairs
nucleic acid
EDNESS: single
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  APPLICATION NUMBER:
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Best Local Similarity
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US-08-634-223-16
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APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: PAN, Li-Zhen
APPLICANT: WALSH, Edward E.
APPLICANT: HEARD, Cheryl Janne
APPLICANT: NEWMAN, ROLland Anthony
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246
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STATE: Virginia
STATE: Virginia
COUNTRY: United States
Z19: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                           48;
                                                                                                                                                                                                                                                                         Score 304.2; DB 1
Pred. No. 1.5e-86;
0; Mismatches 48
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Patent No. 5840298
GENERAL INFORMATION:
APPLICANT: BRAMS, Peter
                  SEQUENCE CHARACTERISTICS:
LENGTH: 705 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOCY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 87.4%;
Matches 333; Conservative
  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                         1..705
                                                                                                                                                                             ; NAME/KEY: CDS
; LOCATION: 1...7
US-08-488-376-16
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US-08-634-223-16
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246 240 306

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Sequence 16, Application US/08634400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 705 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 87.4
Matches 333; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 eccapadececeradecrecerataracerecatecariticaecerecerecerea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GACATCCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTCTCGGAGACAGAGTCACC 120
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                                                                                                                                                                               CONDITER: UILLEGA STATES

ZIP: 22131-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IS Floppy disk
COMPUTER: IS Floppy disk
COMPUTER: IS Floppy disk
COMPUTER: IS Floppy disk
COMPUTER: IS Floppy disk
COMPUTER: IS Floppy disk
COMPUTER: IS Floppy disk
COMPUTER: IS Floppy disk
SUCTAMER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/68,376
FILING DATE: 07-JUN-1995
ATTORNEY AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
TELEPAN: (703) 836-620
TELEPAN: (703) 836-620
TELEPAN: (703) 836-620
TELEPAN: (703) 836-2021
INFORMATION FOR SEQ ID NO: 16:
SEQUIENCE CHARACTER:STICS:
LIENGTH: 705 base pairs
TYPE: MUCLEIC GATA
TYPE: MUCLEIC GATA
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87.4%; Pred. No. 1.5e-86;
iive 0; Mismatches 48
                                ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGACCAAGGTGGAAATCAAA 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 87.4
Matches 333; Conservative
             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1..705
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LOCATION:
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RESULT 12 US-08-634-400-16

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APPLICANT: BRAMS, Peter
APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: PAN, Li-Zhen
APPLICANT: PAN, Li-Zhen
APPLICANT: WALSH, Edward E.
APPLICANT: HEARD, Cheryl Janne
APPLICANT: HEARD, Cheryl Janne
APPLICANT: HEARD, Cheryl Janne
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APPLICANT: HEARD, Cheryl Janne
APPLICANT: HEARD, Cheryl Janne
APPLICANT: HEARD, Cheryl Janne
APPLICANT: HEARD, CHERYPERIN AND
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: BUINS, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 AGGTTCAGCGGCAGTQGATCTCGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCGCT 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: Alexandria
STATE: Virginia
STATE: Virginia
COUNTRY: United States
ZIF: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.6%; Score 304.2; DB 2;
87.4%; Pred. No. 1.5e-86;
tive 0; Mismatches 48;
                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/488,376
FILING DATE: 07-JUN-1995
ATTORNEY AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
FEFERENCE/DOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-620
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LINGTH: 705 base pairs
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```
APPLICANT: CHAMA, Soulaima Salim
APPLICANT: PAN, Li-Zhen
APPLICANT: PAN, Li-Zhen
APPLICANT: WALSH, Edward B.
APPLICANT: HEARD, CHERYJ Janne
APPLICANT: HEARD, CHERYJ Janne
APPLICANT: HEARD, CHERYJ JANDONY
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                 246
186
                                                                                                       240
                                                                                                                                                                                                                                                                                    307 GAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAA 366
                                                                                                                                                                                                                                                                                                                                                                                                301 GAAGATTTTGCAACTTACTATTGTCAACAGGCTTACAGTACCCCCTGGACTTTCGGCCCA 360
                                                                                                                                                                                                                                                          247 AGGTTCAGCGGCAGTGGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCT 306
                                                                                                                                                                                           127 ATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAGAAACCA
                                                                                                                                                                 187 GGAAAAGCTCCTAAGCTCCTGATCTAGCATCCAGTTTGCAAAGTGGGGTCCCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESTONDENCES SON CORREST MATCHIS STREET: P.O. Box 1404
CITY: Alexandria
STATE: P.O. Box 1404
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READANE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,057
FILING DATE: O7-UN-1995
ATTOREY APPLICATION DATA:
APPLICATION NUMBER: US 08/488,376
FILING DATE: 07-UN-1995
ATTOREY APPLICATION NUMBER: US 08/488,376
FILING DATE: 07-UN-1995
ATTOREY ABENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    012712-150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 GGGACCAAGGTGGAAATCAAA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/08770057
Patent No. 5958765
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFRENCE/DOCKET NUMBER: 01271
TELECOMMUNICATION INPORMATION:
TELEPHONE: (703) 836-6620
TELEPAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE: |
FEATURE:
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US-08-770-057-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: MONOCLONAL ANTHBODIES SPECIFIC TO RSV F-PROTEIN AND
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE BUTTHS, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
                                                    GAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAA 366
       241 AGGTTCAGTGGCGGTGGATCTGGGACAGATTTCACTCTCACCATCAACAGTCTGCAACCT 300
                                                                                                301 GAAGATTTTGCAACTTACTATTGTCAACAGGCTTACAGTACCCCCTGGACTTTCGGCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BRAMS, Peter
APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: PAN, Li. Zhen
APPLICANT: MALSH, Edward E.
APPLICANT: MEARD, Cherryl Janne
APPLICANT: NEWANN, Roland Anthony
ITILE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/635,878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,376
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, RObin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-620
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 705 base pairs
TYPE: NUCleic acid
STRANDEDRESS: single
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                             GGGACCAAGGTGGAAATCAAA 387
                                                                                                                                                                                           361 GGGACCAAGGTGGAAATCAAA 381
                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/08635878
Patent No. 595364
GENERAL INFORMATION:
APPLICANT: CHAMAT, Soulaima Salin
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Best Local Similarity 87.4%;
Matches 333; Conservative
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STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
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; LOCATION:
US-08-635-878-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.6%; Score 304.2; DB 3; ilarity 87.4%; Pred. No. 1.5e-86; Conservative 0; Mismatches 48;
                 TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 836-620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 705 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-335-6978-16
                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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Best Local Similarity
Matches 333; Conservat
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APPLICANT: BRAMS.
CHAMAI, Soulaima Salim
PAN, Li-Zhen
PAN, Li-Zhen
WALSH, Edward E.
HEARD. Cheryl Janne
NEWMAN, Roland Anthony
TITLE OF INVENTION: NEUTRALIZING HIGH APFINITY HUMAN
MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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CITY: Alexandria
STATE: Virginia
COUNTRY: United States
                                                                                                                                      DB 2;
                                                                                                                                  Score 304.2; DB 2
Pred. No. 1.5e-86;
0; Mismatches 48
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APPLICATION NUMBER: US/09/335,697B
FILING DATE: 06-Jul-2000
CLASSIFICATION: «Unknown»
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RAPPLICATION WINBER: 08/770,057
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
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ilarity 87.4%;
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; LOCATION:
US-08-770-057-16
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December 29, 2003, 16:08:50 ; Search time 1379.44 Seconds (without alignments) 9875.644 Million cell updates/sec
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333
1_CAGTCTGCCCGACTCAGCC......CCCGGTTGACCGTCCTAGGT 333
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                   OM nucleic - nucleic search, using sw model
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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therapeutic human antibodies and application to functional
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92.5%;
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Best Local Similarity
Matches 308; Conserv
                genomics
Unpublished
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                                                          AUTHORS
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                              JOURNAL
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806 bp mRNA linear PRI 02-JUL-2002
Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
region, partial cds, clone:Ll5.
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Construction and characterization of antibody libraries: isolation
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 KXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                        Direct Submission
Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 20H, UK
Location/Qualifiers
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Pred. No. 5.8e-75;
0; Mismatches 25; Indels
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                                                                                                                                                                                                                                                                                                                                                            102
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/isoTate="donor IT"
/db xref="taxon:9606"
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                                                                                                                                                                                                                           clone="24-17ITIIH34"
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/gene="IGLV"
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92.5%;
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                              J. Mol. Biol.
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Ignatovich,0.
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Matches 308
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Human IG rearranged lambda-chain mRNA V-J-C-region, partial cds.
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/gene="IGL"
/codon ettart=1
/producf="imunoglobulin lambda light chain VLJ region"
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/clone lib="AlMS4"
/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
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Prèd. No. 5.6e-75;
0; Mismatches 25; Indels
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HUMIGLADG
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DEFINITION
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PRI 06-FEB-1997
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241 CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTA 300
                                                                   266 cadecreaddaccaddcradriatracrecadcricararacadgcadcadcrergredra 325
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (O6-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                            HSZ85033 19 lambda light chain variable region gene (24.07IIIIB176) rearranged; Ig-Light-Lambda; VLambda
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Pred. No. 1.7e-74;
0; Mismatches 26;
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/tissue type="peripheral blood"
/clone lib="cDNA library"
                                                                                                                                               301 TTCGGAAGAGGACCCGGTTGACCGTCCTAGGT 333
                                                                                                                                                                                            126 TTCGGCGGAGGACCAAGCTGACCGTCCTAGGT
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/isolate="donor IT"
/db_xref="taxon:9606"
/map="22q11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="24-07ITIIB176"
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ilarity 92.2%;
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146 c
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Homo sapiens
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Ignatovich, O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Mol. Biol.
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                                                                   C-region; J-region; V-region; immunoglobulin lambda; immunoglobulin light chain; processed gene. Homo sapiens (human) Homo sapiens
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/db_xref="G1:186091"
/db_x
                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Mannalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
The anti-DNA associated idiotype 8.12 is encoded by the V lambda III gene family and maps to the vicinity of L chain CDR1
J. Immunol. (1992) In press
Original source text: Homo sapiens (individual_isolate SLE patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCAGTAATCGGCCCTCAGGGGTT 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACCCAGGCAAAGCCCCCCAAACTCATGATTTATGATGTCGCTAAAGCGGGCCTCAGGGGTC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 TCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CAGTCTGCCCCGACTCAGCCTCCCTCTGTCTGGGTCTCCTGGACAGTCGGTCACCATC
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product="immunoglobulin lambda-chain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/isolate="SLE patient PV"
/db_xref="taxon:9606"
/dap="22q11.1-q11.2"
/cell_type="Blymphocyte"
1. 400
/gene="IGL@"
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/gene="IGL@"
/note="G00-128-432"
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Human Ig rearranged lambda chain (V-lambda-2.DS) mRNA, V-, J-, and
C-region subgroup II.
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Paul, B., Livneh, A., Manheimer-Lory, A.J. and Diamond, B.
Characterization of the human Ig V lambda II gene family and analysis of V lambda polymorphism in systemic lupus
                                     180
                                                                                                                                    267 TCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 326
                                                                                                                                                                                                         CAGGCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTA 300
147 TCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAG 206
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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C-region; J-region; V-region; immunoglobulin; immunoglobulin
lambda; immunoglobulin light chain; variable region subgroup II.
                                     CACCCAGGCAAAGCCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC
                                                          TCTGATCGCTTCTCTGGCTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC
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/note="G00-128-432"
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/cell type="B lymphocyte"
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/db_xref="taxon:9606"
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/gene="IGL@"
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franslation="MAWALLLLLTLTCTGSWAQSALTQPASVSGSPQGSITISCTGT
SSDVGGYNYVSWYQDPAKAPKLMIYDVSKRPSGVSNRFSGSKSGNRASLTISGLQAE
DEADYYCSSYTSSSTFVFGGGTKLTVLGQPKAAPSVTLFPPSSEEL"
                                                                                                                                                                     HUMIGLDS 473 bp mRNA linear PRI 29-NOV-1996
Human Ig lambda L chain subgroup II V-2.DS mRNA, VJ region, partial
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 473)

Paul, E., Livrah, A., Manheimer-Lory, A. and Diamond, B.

Characterization of the human immunoglobulin V-lambda-II gene family and analygis of V-lambda-II and C-lambda polymorphism in systemic lupus erythematosus
J. Immunol. (1991) In press

Location/Qualifiers
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/cell_line="EBV-transformed B cell"
/cell_type="B lymphocyte"
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db_xref="GI:186135"
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/isolate="SLE patient D:
/db_xref="taxon:9606"
/chromosome="22"
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/gene="IGL@"
/note="G00-128-432"
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808 bp mRNA linear PRI 02-JUL-2002
Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
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CQVTHBGSTVEKTVAPTECSARQSTPFVCEYQGQSSDLPQPPVNAGGGSGG"
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Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
                                                                                                                                                                                                                                                                                                                                                                                                                                    247 TCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 306
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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/clone_lib="AIMS4"
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/gene="IGL"
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TGTSSDVGGYNYVSWYQQHPGKAPKLMIYDVSKRPSGVSNRFSGSKSGNTASLTISGL
QAKDEADXYCSSYTSSSTWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVÇ
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Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
  TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 120
                                                                                                                                                                        TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGGCTC 240
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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'protein id="BAC01780.1"
'db_xref="GI:21669511"
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/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
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Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University,
Kutsukake-cho, Toyoake 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
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Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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TGTSSDVGTNYVSNYQQHPGKAPELMIYDVSKRPEGGVSGNTASLTISGL
ABDBADYYCSSYTGSSTWYPYGGGFKLTVLGQPKAAPSVTLFPPSSELQANKATLVC
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Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/protein_id="BAC01792.1"
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/note="mixture of tissues:tonsils, umbilical cords, peripheral blood and bone marrow"
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Kurosawa,

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/tränslation="QSALTQPASVSGSPGQS1T1SCTGTSSDVGGYNYVSWYQQHPGK
APKLMTYDVSKRPSGVSNRFSGSKSGNTASLT1SGLQAEDEADYYCSSYTSSSSWVFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGLV gene, immunoglobulin lambda chain; immunoglobulin light chain; variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TCCTGCACTGGAACCAGGGATGACGTTGGTGCTTATAACTATGTCTCCTGGTACCAACAA 120
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                     <1. .>333
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/codon start=1
/product="immunoglobulin lambda light chain VLJ region"
/protein id="BAC01652.1"
/db_xref="GI:21669255"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CAGTCTGCCCCGACTCAGCCTCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATC
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                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
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/clone="lib="AIMS4"
/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsukake-cho, Toyoake 470-1192, Japan (E-mail:kurosawa@tijita-hu.ac.jp, Tel:81-562-93-9387) Please visit our web site URL:http://www.fujita-hu.ac.jp/immunity/.
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Pred. No. 5.1e-74;
0; Mismatches 27
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                                                                                                                                                                                   1. .333
/organism="Homo sapiens"
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91.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                gene="IGL"
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Homo sapiens
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Matches 306; Conservative
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AUTHORS
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PRI 02-JUL-2002

linear

mRNA

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SOURCE
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                  Thyroid peroxidase autoantibodies obtained from random single chain FV libraries contain the same heavy/light chain combinations as
                                                                                                                                                                                                                                                                                                                                                                                               note="Anti-thyroid peroxidase scFv fragment isolated from phage display combinatorial library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /trānslation="QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGK
APKLMIYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTSSSTRVFG
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                                                                                                                                                         Direct Submission
Submitted (05-JAN-2000) Chapal N., Faculte de Pharmacie, CNRS
UMR9921, 15 avenue Charles Flahault, Montpellier 34060, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="immunoglobulin lambda chain variable region"
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102 c 84 g 78 t
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                                                                                                                                                                                                                                                                                                                          cell_type="Thyroid infiltrating B cells"
clone_lib="panB library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 289.8; DB 9;
Pred. No. 5.1e-74;
0; Mismatches 27;
                                                                     Endocrinology 142 (11), 4740-4750 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein_id="CACO6678.1"
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                                                                                                                                                                                                                                                     organism="Homo sapiens"
Bouanani, M. and Peraldi-Roux, S
                                                                                                                                                                                                                                                                                        db_xref="taxon:9606"
clone="B10"
                                                                                                                                                                                                                   location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                country="France"
                                                                                                                                                                                                                                                                       mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="IGLV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="IGLV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="IGLV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tch 87.0%; al Similarity 91.9%; 306; Conservative
                                                                                                                                                                                                                                                                                                                                                                 rearranged
                                                                                                                         2 (bases 1 to 333)
Chapal, N.
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                                                        occur in vivo
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Best Local S
Matches 306
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ORIGIN
                                                                       JOURNAL
MEDLINE
PUBMED
                                                                                                                         REFERENCE
AUTHORS
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                    TITLE
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RESULT 11 AB064163

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/trānslation="MKYLLPTAAAGLLLLAAQPAMAQSALTQPASVSGSPGQSITISC
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CQVTHEGSTVEKTVAPTECSARQSTPFVCEYQGQSSDLPQPPVNAGGGSGG"
                                                                                                                                                                                                                                        Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M., Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J., Multa,K. and Kurosawa,Y.
Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/producie="immunoglobulin lambda light chain VLJ region"
/protein_id="PAC01791.1"
/db_xref="GI:21669533"
             Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ region, partial cds, clone:L23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="mixture of tissues:tonsils, umbilical cords, peripheral blood and bone marrow"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (25-JJN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsukake-cho, Toyoake 470-1192, Japan (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387) Please visit our web site URL:http://www.fujita-hu.ac.jp/immunity/.
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0; Mismatches 27;
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254 c 215 g 164 t
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810 bp
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/db_xref="taxon:9606"
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                                                                                         AB064163.1 GI:21669532
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/gene="IGL"
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ilarity 91.9%;
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/gene="IGL"
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Unpublished
2 (bases 1 to 810)
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Best Local Similarity
Matches 306; Conserv
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HSZ85382
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/protein.id="BAC01628.1"
/db xref="d1:21669207"
/translation="QSALTQPASVGGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGK
APKLMIYDVSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTSSSTYVFG
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Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
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                                                  307 CAGGCTGAGGACGAGGCTGATTATTACTGCAGCTCATATACAAGCAGCAGCTCTTGGGTG 366
                                CAGGCTGAGGACGAGGCTGATTATTACTGTTCTTCATATACAACCAGTAGCACTTTGTTA 300
247 TCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 306
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyoake 470-1192, Japan
(B-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.
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Pred. No. 1.5e-73;
0; Mismatches 28; Indels
                                                                                                                  367 TTCGGCGGAGGACCAAGCTGACCGTCCTAGGT 399
                                                                                                TTCGGAAGAGGACCCGGTTGACCGTCCTAGGT 333
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L129"
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Best Local Similarity 91.6%;
Matches 305; Conservative (
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/gene="IGL"
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Kurosawa, Y.
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                                                                                                                                                                                                                                DEFINITION
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AB064000
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HSZ85382 19 lambda light chain variable region gene (34-095WIIC37) rearranged; Ig-Light-Lambda; VLambda.
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                                                                                                                                                             CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGCCTCAGGGGTC 180
                                                                                                                                                                                                                        CAGGCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTA 300
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61 TCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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20H, UK
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antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
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Pred. No. 1.5e-73;
0; Mismatches 28;
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/tissue type="peripheral blood"
/clone lib="cDNA library"
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                                                                                                                                                                                                                                                                                                                                                     Treggacreagercaccerectager 333
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Submitted (06-FEB-1997) Ignatovich O.,
Engineering, Hills Road, Cambridge CB2
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/mol type="genomic DNA"
/isolate="donor SW"
/db xref="taxon:9606"
/map="22011.2"
/clone="34-09SWIIC37"
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nilarity 91.6%;
Conservative 0,
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Homo sapiens
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J. Mol. Biol.
2 (bases 1 to 375)
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Best Local Similarity
Matches 305; Conserv
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/trānslation="MAWSPLFLFLLTQGTGSWAQSALTQPASVSGSPGQSITISCTGT
SSDVGGYNYVSWYQQHPGKAPKLMIYDVSNRPSGVSNRFSGSKSDNTASLTISGLQAE
DEADYYCSSYTSSSTLVFGGGTKLTVIR"
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Human immunoglobulin light chain variable region mRNA, cell line
113elo, anti-RhD, partial cds.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 453)
Boucher, G., Broly, H. and Lemieux, R.
Restricted Use of Cationic Germline VH Gene Segments in Human Rh(D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (21-DEC-1995) Gerard Boucher, Research and Development, The Canadian Red Cross Society, Transfusion Center of Quebec, 2535 Laurier Boulevard, Ste-Foy, Quebec GlV 4M3, Canada Location/Qualifiers
                                                                                                                                  298 CAGGCTGAGGAGGCTGATTATTACTGCCTCATATACAAGCAGCAGCACTCTCGTC 357
178 CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCAGTAATCGGCCCTCAGGGGTT 237
                                                                                                             241 CAGGCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTA 300
                               181 TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC
                                                                          238 TCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC
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note="Rhesus blood group antibody V region"
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protein id="AAB01806.1"
db_xref="GI:1353830"
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/product="Ig light chain variable region"
58. .123
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/organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/cell line="heterohybridoma:13el0"
/cell type="leukocytes"
/note="rearranged"
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                                                                                                                                                                                       TTCGGAAGAGGACCCGGTTGACCGTCCTAGGT
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358. .390
/note="encodes FR4"
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H.sapiens Ig lambda light chain variable region gene (25-28SWIID60)
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                       121 CACCCAGGCAAAGCCCCCAAACTCATGATTATGATGTCAGTAATCGGCCCTCAGGGGTT 180
                                                                          TCTGATCGCTTCTCTGGCTCCCAACACGGCCTCCCTGACGTCTCTCTGGGCTC 240
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                                                                                                                                                    CAGGCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTA 300
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XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
Repertoire
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 20H, UK
Location/Qualifiers
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antigen receptor; immunoglobulin; immunoglobulin light chain; immunoglobulin superfamily; rearranged; variable region. Homo sapiens
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ftissue type="peripheral blood"
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91.6%; Pred. No. 1.5e-73;
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Ignatovich,0.
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                                                                  0; Gaps
                                      Score 288.2; DB 9; Length 453;
Pred. No. 1.5e-73;
0; Mismatches 28; Indels 0;
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Search completed: December 29, 2003, 19:01:21 Job time : 1380.44 secs

AV697043 AV697043 BX280395 BX280395 AV699040 AV699040 CD101742 AGENCOURT AV685070 AV685070 B1820758 603034354 BG685732 602637827 BG756493 602439065 BG756493 602503383

AW406701 UI-HF-BLO BG059377 nah50e11. AW404692 UI-HF-BLO BG759257 602710936

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Database

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BE975970 880 bp mRNA linear EST 22-JAN-2001
602246174F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4337226 5',
mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov. c column: 19
Plate: LLCM1211 row: c column: 19
High quality sequence stop: 759.
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                                                                                                                                                                                                                                                              BG397577
AV686421
BG564971
BG566373
BM831030
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BM830988
BM773502
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BG483745
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BG756874
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BF975970 602246174
BM914350 AGENCOURT
AV694861 AV694861
AV693754 AV693754
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1 CAGTCTGCCCCGACTCAGCC......CCCGGTTGACCGTCCTAGGT 333
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                                                                                                                                                                                                                                         45562784
           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                 22781392 seqs, 12152238056 residues
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Maximum Match 100%
Listing first 45 summaries
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BM914350
AV694861
AV693754
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                                                          nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Score

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BM007694 603617126 BGS41853 602569746 AM40505B UI-HF-BL0 BGS36723 602564852 BQ712542 AGENCOURT

AW404544 UI-HF-BL0

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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (Dases 1 to 710)
Xiao, H., Gu, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
Hu, G., Gu, J., Chen, Z. and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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85.6%; Score 285; DB 12; Length 1078;
Best Local Similarity 91.0%; Pred. No. 1.5e-69;
Matches 303; Conservative 0; Mismatches 30; Indels 0;
found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM2002 row: d column: 03 High quality sequence stop: 538.
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                                                                                                                                                                                                           /tissue type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clocallb="NHH MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAGG(G). Size-selected >500bp for average innert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NHH MGC Library."
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NIH-MGC http://mgc.nci.nih.gov/.
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Contact: Robert Strausberg, Ph.D.
Email: Gapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGGCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTA
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Pred. No. 2.1e-71;
0; Mismatches 26; Indels
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                                                                                       organism="Homo sapiens"
                                                                                                                                                                                          /clone="IMAGE:4337226"
                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
                     Location/Qualifiers
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Homo sapiens
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Matches 307; Conservative
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AV697043 AKC Homo sapiens cDNA clone GKCGWG01 5', mRNA sequence.
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(Dases 1 to 767)

Xu,X.; Huang,J.; Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Chen,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.

Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
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                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="GKC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hang@chgc.sh.cn
Email: hang@chgc.sh.cn
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/dev_stäge="Adult"
/lab_host="SOLR"
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="GKCGWD05"
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90.4%;
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Mammalia; Butheria; Primates, Catarrhini, Hominidae, Homo.
               Contact: Zeguang Han
Contact: Zeguang Han
Contact: Zeguang Han
Johnsee National Human Genome Center at Shanghai
151 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801912
Fax: 86-21-50801922
Fax: 86-21-50801922
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GKCGWE01"
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BX280395 Soares multiple sclerosis 2NbHMSP Homo sapiens cDNA clone IMAGp998E24628; IMAGE:283391, mRNA sequence.
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1 (bases 1 to 485)
Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B.
Human UnigeneSet - RZPD3
                                                                                                                                                                                                                                                                       /clone_lib="GKC"
/note="Vector: pBluescript sk(-); Site_1: BcoRI; Site_2:
                                      Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
315 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
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dev stage="Adult"
lab_host="SOLR"
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'organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="GKCGWG01"
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Contact: Ina Rolfs
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RZPDILB; I.M.A.G.E. cDNA Clone Collection;
RZPDILB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/Cgi-
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzeatrum fuer Genomforschung GmbH
Reubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 111
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (cloneGrzpd.de) for further information. Seq primer:
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissum.trpe="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Sosses multiple_sclerosis 2NbHMSP"
/note="Vector: pT773D (Pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not 1; Site_2: Eco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 TCTGATCGCTTCTCTCGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC
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RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 280.2; DB 13; Length
Pred. No. 2.3e-68;
0; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="1MAGp998E24628 ; IMAGE:283391"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trcggaacrggaccaaggrcaccgrccraggr 409
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                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"<sup>.</sup>
                                                 RZPD; IMAGD998E24628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 90.1%;
Matches 300; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="male"
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/organism="Homo sapiens"

/mol_type="mRNA"

/db_txef="lawaon:9606"

/clone="IMAGE:3034479"

/tissue_type="Human Placenta"

/lab_host="DHIHOB TonA"

/clone_lib="NIH MGC_147"

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/note="Organ: placenta; Vector: pBluescriptR; Site_1:

/note="Organ: placenta; Vector: pBluescriptR; Site_1:

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                         CD101742
AGENCOURT_13902002 NIH_MGC_147 Homo sapiens cDNA clone
IMAGES30347479 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbe-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LinL at:
http://mage.lnn.gov
Plate: NDAM388 row: k column: 08
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 766)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 cccccadecacaccccccaaacrcarcarrarrargaercagrarrcecccrcaggerc
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                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 14; Length 766;
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Pred. No. 2.9e-68;
0; Mismatches 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 585. Location/Qualifiers
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Best Local Similarity 90.1%;
Matches 300; Conservative (
                                                                                                                                                                                                                       Homo sapiens (human)
Homo sapiens
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                     ACCESSION
                                                                                                                                                                 VERSION
KEYWORDS
               CD101742
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                                                                                                                                                                                    SM Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver

AL Proc., Natl., Acad., Sci. U.S.A., 98 (26), 15089-15094 (2001)
AV699040 GKC Homo sapiens cDNA clone GKCGXE07 5', mRNA sequence.
AV699040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBluescript sk(-); Site 1: EcoRI; Site 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTC
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0
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/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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Pred. No. 2.9e-68;
0; Mismatches 33
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/db_xref="taxon:9606"
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// db_xref="taxon:9606"
// clone="rakabe:15684"
// lab host="mbH108"
// lone lib="NIH MGC 115"
// lone lib="NIH MGC 115"
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// lone lib="NIH MGC 115"
// lone lib="Organ: pooled brain, lung, testis; Vector:
// note="Organ: pooled brain, lung, testis; Vector:
// note="Organ: pool of 6 male brains, age range 23-27; lagorce anonymous pool of 6 male brains, age 69. Library is
// soligo-dT primed and directionally cloned (Econv site is
// oligo-dT primed and directionally cloned (Econv site is
// oligo-dT primed and directionally cloned (Econv site is
// destroyed upon cloning). Average insert size 1.8 kb,
// insert size range 1-3 kb. Library is normalized and
// enriched for full-length clones and was constructed by C.
// Gruber (Invitrogen). Research Genetics tracking code
// 15 a 259 c 207 g 146 t
                                                                                                                                                                                     787 bp mRNA linear EST 04-OCT-2001
60304354F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175684 5',
mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to ?787)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Righte: LiAM11437 row: k column: 13
High quality sequence start: 2
High quality sequence stop: 785.
High quality sequence stop: 785.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 2.9e-68;
0; Mismatches 33;
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333
                                   386 TTCGGCGCAGGACCAAGCTGACCGTCCTAGGT
   301 TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT
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Contact: Robert Strausberg, Ph.D.
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/organism="Homo sapiens"
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Homo sapiens
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1 (bases 1 to 788)

Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Pax: 86-21-50801922
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84.1%; Score 280.2; DB 9; Length
Best Local Similarity 90.1%; Pred. No. 2.9e-68;
Matches 300; Conservative 0; Mismatches 33; Indels
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/mol_type="mRNA"
/db xref="taxon:9606"
/clone="GKCGXG07"
/rissue_type="hepatocellular carcinoma"
/dev stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai
Location/Qualifiers
   TTCGGCGGAGGGACCAAGCTGACCGTCCTAGGT 458
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/Lissue type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/clone lib="NHI MGC 48"
/note="Organ: NHI MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: Xho1;
Site_2: BcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/Xho1 sites using the following 5' adaptor: GGACGGGG(G). Size-selected >500bp for average insert size 1.8kb. Library, constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis Kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NHHMGC Library."
                                                                                                                                                                                                                                                                                                                                                                              BG397282 112-MAR-2001
602439065F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565272 5',
                                                                                                CAGGCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTA 300
                                                                                                                             329 CAGGCTGAGGATGATGATTATTACTGCAGCTCATATGCAGCAGCAGCAACACTTATGTC 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contract: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1282 row: a column: 17
High quality sequence stop: 840.
Location/Qualifiers
                                             269 céréarésérréreresérecaasrereséaacacacérecereségerereségere
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181 TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 840)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                   TTCGGAAGAGCCCCGGTTGACCGTCCTAGGT
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/db_xref="taxon:9606"
/clone="IMAGE:4565272"
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/lab host="DH10B (phage-resistant)"
/clocallb: "DH10B (phage-resistant)"
/clocallb: "DH10B (phage-resistant)"
/clocallb: "DH10B (phage-resistant)"
Site 2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIY/Kho! sites wisng the Directionally cloned into EcoRIY/Kho! Size-selected >500pp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAB-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: Libis is a NIH MGC Library."
                                                                                                                                                                                                                                                                                 BG685732 829 bp mRNA linear EST 01-MAY-2001
602637827F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4765447 5',
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                                             cadecrdadeargaegergarrarracrdeagercararacagedageageaarrragra 388
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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                                                                                                     TTCGGAAGAGGACCCGGTTGACCGTCCTAGGT
                                                                                                                                             389 TTCGGCGGAGGACCAAGGTGACCGTCCTAGGT
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/db_xref="taxon:9606"
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/mol_type="mRNA"
/db xref="texaon:9606"
/clone="IMMGE:485593"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab host="Publio" (phage-resistant)"
/lab host="blio" (phage-resistant)"
/clone lib="NIH MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhOI;
Site_2: E.coRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following S' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
(Strategene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                           BG756493 843 bp mRNA linear EST 15-MAY-2001
602715633F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4855593 5',
                                                                                                                                             CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTA 300
                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
http://image.lln.gov
Plate: LLCM1705 row: b column: 10
High quality sequence stop: 838.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 843)
CACCCAGGCAATGCCCCCCAAACTCATGATTTATGAAGTCACTAATCGGCCCTCAGGGGTT
                                                          TCTGATCGCTTCTCGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC
                                                                                                    rerearceerrereacreeasterescaacacacaceecerecaacareresseere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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                                                                                                                                                                                                                                                        TTCGGAATTGGGACCAAGGTCACCGTCCTAGGT 381
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BG756493
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Matches 300; Conser
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/WOLLY TYPE="MRNA"

/ Ab Xref="taxon:9606"
/ Clone="INARA"
/ Ab host="NARA"
/ Lab host="NARA"
/ Lab host="NARA"
/ Lab host="NARA"
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602503383F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4616829 5',
                                                                                                                                                                                                                            270
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TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 120
                                                                                                                                                       180
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                     271 CCTGATCGCTTCTCTGGGGTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 834.
                                                                                                                                                                                                                                                                                                              181 TCTGATCGCTTCTGGCTCCAAGTCTGGCAACACGCCTCCCTGACCATCTCTGGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 CAGGCTGAGGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTGTTA
                                                                                                                                                           CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC
                                                                                                                                                                                                                                    211 cccccaggcacagcccccaaacrcargarrrargaggrcagrrarcgcccrcagggcc
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 3.1e-68;
0; Mismatches 33; 1
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90.1%;
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Best Local Similarity 90.1
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/cell type="germinal center B cells"
/cell line="MGC85"
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UI-HP-BLO-ada-d-08-0-UI.rl NIH MGC_37 Homo sapiens cDNA clone
IMAGE:3060903 S', mRNA sequence.
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                                               CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATC 156
                                                                                                                                                                                                                                                                                                         CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC 180
                                                                                                                                                  TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.

Email: cgapbs-romail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the T.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image.image.html

Seq primer: M13 Porward.
CAGTCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGGACAGTCGGTCACCATC
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/mol_type="mRNA"
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/clone="IMAGE:3060903"
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Query Match

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                                                                    7 GCCCCGACTCAGCCTCCCTCTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCCTGC
                       Gaps
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                       Indels
                       30;
  Pred. No. 4.7e-68;
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90.8%;
  Best Local Similarity 90.8
Matches 297; Conservative
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Anti-human CD23 6G
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Nucleotide sequenc
Nucleotide sequenc
APRIL binding sCFv
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Nucleotide sequenc
Human autoantibody
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/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:
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'SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:
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'SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:
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| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985_DAT:
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a DNA sequence encoding the light chain variable region of primate monoclonal antibody anti-buman CD23 dGS. The invention provides primate monoclonal antibodies which specifically bind human CD23, the low affinity receptor for 1gE (FceRii/CD23), and comprise either of a human gamma-1 or human gamma-3 constant region that binds to human Fc gamma receptors and inhibits 1gE expression. The monoclonal antibodies of the invention are claimed to be useful for inhibiting induced 1gE production for treating or preventing conjunctivitis, autolammune has meanlytic anaemia, etc. (Updated on 25-WAR-2003 to correct PR field.)
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               *tag= e
note= "encodes CDR 2 region"
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Matches 333; Conservative
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misc_feature
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The invention relates to an isolated polynuclectide (I) encoding a polyneptide (II) comprising a portion of a colon tumour protein. A new oligonuclectide (III) that hybridises to (I) is useful for algonuclectide (III) that hybridises to (I) is useful for determining the presence of a cancer in a patient. (II) or antigen color at tumour protein, by contacting T cells specific for a tumour protein, by contacting T cells with (I), (II) or antigen-presenting cells that express (I). (I), (II), or antigen-presenting cells that express (I). (I), (II), or antigen presenting cells that express (II), so that T cells proliferate, and administering to the patient an effective amount of the proliferated T cells, thus inhibiting the effective amount of the proliferated T cells, thus inhibiting the effective amount of the proliferated T cells, thus inhibiting the cellentual and patient. (I) or (II) is useful for stimulating an immune response in a patient. (I) or (II) is useful in vaccines and pharmaceutical compositions for prevention and treatment of colon cancer and for the diagnosis and monitoring of the cancers (I), (II) or an antibody against (II) is useful as a probe or primer for nucleic acid hybridisation, and in the design and preparation of ribozyme molecules for inhibiting expression of (II) in tumour cells. ABK21975-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      v isolated polynucleotide encoding a polypeptide comprising a portion colon tumour protein, for detection, diagnosis and therapy of human
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                                                                                                                                                                                         Human; colon adenocarcinoma; colon cancer; tumour; gene; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 605 BP; 123 A; 198 C; 154 G; 128 T; 2 other;
                                                                                                                                                 Colon adenocarcinoma-specific cDNA #264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 181-182; 211pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secrist
                                     BP.
                                   ABK29738 standard; cDNA; 605
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22-NOV-2000; 2000US-252614P.
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                                                                                                             (first entry)
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Best Local Simi]
Matches 304; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  colon cancer
                                                                                                             23-APR-2002
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                                                                       ABK29738;
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RESULT 2
                 ABK29738
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anti-MUC1 ScFv, and the second polypeptide

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The specification describes a method for the intracellular analysis of a target molecule within a biological cell. The method comprises expressing within the cell a first polypeptide sequence comprised of a first reporter species capable of binding to the target molecule and a first reporter molety attached to the first binding species; expressing within the cell a second polypeptide sequence comprised of a second binding species capable of competing with the target molecule for binding species capable of competing with the target molecule for binding species capable of competing with the target molecule for binding of the first binding of competing with the target molecule for binding of the first and second binding species the first and second reporter moleties being such that on binding together of the first and second binding species the first and second reporter moleties being species the first and second reporter moleties capable of being generated when the first and second reporter moleties of onc interact; and effecting a measurement to determine the presence capable of being generated when the first and second binding species. The method is useful for the intracellular analysis of a target molecule, e.g. for detecting the presence and/or amount of target capable capable of binding of also useful for studying the circules in calls. The method is also useful for studying the circules in calls. The method is also useful for the MICI epitope of human mucinl, demonstrating the method of the invention. In this assay,
                                           240
TCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 329
                                                                                               CAGGCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTA 300
                                                                                                                          CAGGCTGAGGACGAGGCTGATTATTACTGCAGCTCATATACTAGCATCATCACTGTGGTA 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Intracellularly analysing or detecting the presence of a target molecule within a biological cell, by determining the presence or signal representative of binding of polypeptide species to the target
                                                                                                                                                                                                                                                                                                                                                               Intracellular analysis; intracellular interaction; intrabody; ScFv; MUC1; mucin 1; pScFv-ECFP2; ss.
                                                                                                                                                                      TTCGGCGGAGGACCAAGGTGACCGTCCTAGGT 422
                                                                                                                                                      TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 333
                                                                                                                                                                                                                                                                                                                                        Nucleotide sequence of plasmid pScFv-ECFP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Page 29-31; 51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYMA-) UNIV VICTORIA MANCHESTER.
                                                                                                                                                                                                                                                     BP.
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                                                                                                                                                                                                                                                                                                            28-MAR-2003
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               210
                                                                     270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1158 CACCCAGGCAAAGCCCCCAAACTCATGATTTATGAGGTCAGTAAGCGGCCCTCAGGGGTC 1217
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                                                                                                                                                                                                                                                                                      1038 chárcrácrcráncrcháccracararacarárcaáararacarandaranarachara 1097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 TCTGATCGCTTCTCTGGCTCCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CACCCAGGCAAAGCCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTTC
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Intracellular analysis; intracellular interaction; intrabody; ScFv; MUC1; mucin 1; pBudMUC-EYFPscFvECFP; ss.
the first polypeptide is an anti-MUC1 ScFv, and the second polype; comprises the MUC1 epitope attached to yellow fluorescent protein
                                                                                                                                                                                    .;
0
                                                                                                                          Score 284; DB 25; Length 5464; Pred. No. 1e-78; 0; Mismatches 30; Indels 0.
                                                                            Sequence 5464 BP; 1294 A; 1485 C; 1468 G; 1217 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of plasmid pBudMUC-EYFPscFvECFP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCGGAAGAGGACCCGGTTGACCGTCCTAGG 332
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                                                                                                                             Match 85.3%;
Local Similarity 91.0%;
nes 302; Conservative (
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                                                                                                                                     Query Match
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Matches
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species capable of binding to the target molecule and a first reporter moiety attached to the first binding species; expressing within the cell capable of capable of competing with the target molecule for binding species appable of competing with the target molecule for binding species capable of competing with the target molecule for binding species capable of competing with the target molecule for binding species and a second reporter moiety, the first and second reporter moieties being such that on binding together of the first and second contract so as to be capable of producing a signal that can be differentiated from one capable of baing generated when the first and second reporter moieties on the capable of baing generated by the first and second binding continteract; and effecting a measurement to determine the presence or signal representative of binding of the first and second binding species. The method is useful for the intracellular analysis of a target molecule in cells. The method is also useful for studying the interactions of intracellular molecules. The present sequence represents interactions of intracellular molecules. The MUCI selecting the method of the invention. In this assay, the first polypeptide is an anti-MUCI ScFV, and the second polypeptide comprises the MUCI epitope attached to yellow fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4365 TCCTGCACTGGAACCAGCAGTAGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAG 4424
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APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta; dermatological; immunosuppressive; antialfammatory; antirheumatic; antiarthritic; cytostatic; antiamemic; antiallergic; antiasthmatic; neuroprotective; ophthalmological; tubercallostatic; antidiabetic; antipsoriatic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic; antidammatory disorder; autoimmune disease; graft versus host disease; GVHD; inflammatory disorder; proliferative disorder; single chain antibody; antibody; gene; ss.
                                                 4605 TTCGGCGGAGGGACCAAGGTCACCGTTCTAGG 4636
          TTCGGAAGAGGGACCCGGTTGACCGTCCTAGG 332
                                                                                                                                                                                                                                                                      APRIL binding scFv A027All encoding DNA.
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                                                                                                                                                ABZ25504 standard; DNA; 726
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          301
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                                                                                                       RESULT 5
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Synthetic

4545 CAGGCTGAGGACGAGGCTGATTATTACTGCAGCTCATATAGAAGCAGTAACACTTGGGTG 4604

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The invention relates to a novel antibody or its fragment, which immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL). The antibody of the invention has dermaclogical, immunosuppressive, antiantabedy of the invention has dermaclogical, immunosuppressive, antialtammatory, antiarthratic, cytostatic, antianamic, antianamic, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, antialta, anti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                514 CACCCAGGCAAAGCCCCCAAACTCATGATTTATGAGGGCAGTAAGCGGCCCTCAGGGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated antibody that immunospecifically binds tumor necrosis factor delta, useful for treating, preventing or ameliorating Orn-Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.1%; Score 283.4; DB 25; Length
90.7%; Pred. No. 7.5e-79;
tive 0; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 726 BP; 156 A; 199 C; 220 G; 151 T; 0 other;
                                                                      /product= "A027A11 scFv"
/note= "No start/stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 192; 225pp; English
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunospecifically bind to APRIL.
                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                               22-MAY-2002; 2002WO-US16106.
                                                                                                                                                                                                                                                                                            24-MAY-2001; 2001US-293100P.
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Matches 302; Conservative
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P-PSDB; ABP60522.
                                                                                                                                               WO200294192-A2
                                                                                                                                                                                               28-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                              Ry upen SM;
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     Key
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fragment. The fragment is used to produce a mixture or panel of 5
different specific binding members, each comprising an antibody VH
and/or VL variable domain and capable, when displayed on the surface
of filamentous bacteriophage particles or in the case of a specific
binding member comprising the DS VH and/or VL variable domain when
bood brain barrier (BBB). The panel is useful for the selection of
specific binding members with a desired property such as ability to
cross BBB, ability to bind endothelial cells or other brain cell antigen,
ability to bind intracellular adhesion molecules and to bind transferrin
receptor. The antibodies are useful in diagnosis, prophylaxis and
treatment of human or animal body, including neurological diseases, such
as Alzheimer's disease, prion disease, AIDS-related dementia, epilepsy
and traumatic brain injury and any diseases involving inflammation
cocurring within the brain or central nervous system.
TCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACAATCTCTGGGCTC 633
                                                                                               CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTA 300
                                                                                                                                   CAGGCTGAGGACGAGGCTGATTATTACTGCAGCTCATATACAACCAGGAGCACCTCGAGTT 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody; light chain; VL; amyloid protein; blood brain barrier; endothelial cell; brain cell antigen; inflammation; adhesion molecule; transferrin receptor; neurological disease; Alzheimer's disease; prion disease; Albeimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mixture or panel of antibodies for selecting specific binding members that cross the blood brain barrier, for use in delivering different molecules and treating neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide sequence of variable light chain fragment of clone. G93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.3%; Score 280.8; DB 22; Length 90.4%; Pred. No. 3.7e-78; ive .. 0; Mismatches 32; Indels
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                                                                                                                                                                                                                                                             TTCGGCGGAGGACCAAGCTGACCGTCCTAGGT 726
                                                                                                                                                                                                                            TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH42401 standard; DNA; 333
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Best Local Similarity 90.4<sup>†</sup>
Matches 300; Conservative
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P-PSDB; AAG62957.
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                                                                                                                                                                                                                                                                                                         CAGGCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTA 300
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                                                                                                                                                                                        CACCCAGGCAAAGCCCCCAAACTCATGATTTATGAGGGCAGTAAGCGGCCCTCAGGGGTT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody, light chain; VL; amyloid protein; blood brain barrier; endothelial cell; brain cell antigen; inflammation; adhesion molecule; transferrin receptor; neurological disease; Alzheimer's disease; prion disease; Alzheimer, sinjury; ss.
                                                                          TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC
                                                                                                                                                    CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC
                                                                                                                                                                                                                                                    TCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACAATCTCTGGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mixture or panel of antibodies for selecting specific binding members that cross the blood brain barrier, for use in delivering different molecules and treating neurological diseases
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                                  cagrererereacticaectrecererereresererecteeresereseresereseresere
                                                                                                                                                                                                                              TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTTGGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes an antibody variable light chain (VL) fragment. The fragment is used to produce a mixture or panel of 5 different specific binding members, each comprising an antibody VH and/or VL variable domain and capable, when displayed on the surface of filamentous bacteriophage particles or in the case of a specific binding member comprising the D5 VH and/or VL variable domain when bound to human serum amyloid protein, to pass through a mammalian blood brain barrier (BBB). The panel is useful for the selection of specific binding members with a desired property such as ability to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence of variable light chain fragment of clone G102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chain; VL; amyloid protein; blood brain barrier;
                                                                                                                                                                                                                                                                                                                                                                                                                         rrceccesaeceaaccaaecreaccerceraec 332
                                                                                                                                                                                                                                                                                                                                                                                       TTCGGAAGAGGGACCCGGTTGACCGTCCTAGG 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 106; 109pp; English.
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90.4%; Pred. No. 3.7e-78;
ive 0; Mismatches 32;
                                                                                                                                                                                                                                                                                Sequence 333 BP; 72 A; 99 C; 86 G; 76 T; 0 other;
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This invention describes a novel fusion protein (I) that has, at its N-terminus, one or more epitopes that bind specifically to autoantibodies (AAb) against the islet cell antigen IAA2 and, at its C-terminus, one or more epitopes that bind specifically to antibodies (Ab) directed against the glutamate decarboxylase GAD65. (I), also nucleic acid (II) encoding the yectors containing (II) and transformed cells, are useful for diagnosis and prognosis of diabetes mellitus type 1, stiff—man syndrome, polyglandular autoimmune syndrome or other autoimmune conditions associated with AAb against GAD65 or IA2. (I) provides a rapid and simple diagnosis of high specificity and sensitivity, capable of recognizing antibodies against both IA2 and GAD65, simultaneously. Unlike known fusions, where the GAD65 component is at the N-terminus, (II) contains correctly folded conformational epitopes that can react with most MICA autoantibodies. This sequence encodes the human autoantibody MICA-1 variable region heavy chain used in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACTCAGCCTGCCTCCGTGTCTCGGTCTCGACAGTCGATCACCATCTCCTGCACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 AACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCACCCAGGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
              metabolic diseases, is reactive with autoantibodies against both
glutamate decarboxylase and islet cell antigen
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                                                                                                                                                                                                                                                                                                                                                                                                        / Match 84.2%; Score 280.4; DB 22; Length 351; Local Similarity 91.9%; Pred. No. 5e-78; nes 296; Conservative 0; Mismatches 26; Indels 0;
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fusion protein, useful for diagnosis of diabetes
                                                                                                                                                                                                                                                                                                                                                                          Seguence 351 BP; 71 A; 106 C; 91 G; 83 T; 0 other;
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                                                                      Disclosure; Page 22; 68pp; German
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19-JUL-2001; 2001WO-GB03252. 19-JUL-2000; 2000GB-0017720

NO200208263-A2 31-JAN-2002 GOT-A-GENE AB.

(GOTA-) (GARD/)

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The present sequence encodes a recombinant human antibody scFv. Antibody TN11 reacts with the long form of human Tenascin-C (TN-C). The epitope recognised by TN11 is located inside domain C of TN-C. TN11 is therefore only capable of recognising TN-C isoforms containing domain C (CTN-C). TN11 is useful for detecting the presence of TN-C isoforms in vitro or in vivo for diagnosing pathologies expressing the CTN-C isoforms of TN-C. It is useful for the preparation of formulations for the treatment of
                                                                                                                                                                                                       of
                                                                                                                                                                                   Ligands used for diagnosis and treatment of human neoplasias, are capable of identifying the tenascin-C isoform containing domain C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 747 BP; 157 A; 197 C; 231 G; 162 T; 0 other;
                                                                                                                                                                                                                                                             Claim 8; Page 5-6; 31pp; English
                   99IT-FI00094.
                                                      (PHIL-) PHILOGEN SRL
                                                                                                                             WPI; 2000-687225/67.
P-PSDB; AAB36083.
                                                                                                                                                                                                                                                                                                                                                                                                                                 human neoplasias.
                   20-APR-1999;
                                                                                                                                                                                                                          tenascin-C -
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Best Local Similarity 90.1%;
Matches 300; Conservative 415 ( 241 301 475 535 181 595 655 61 121 셤 8 용 6 음 중 . <del>G</del> ò ò 유 ð 셤

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Modified virus; cytostatic; gene therapy; tumour cell; problierating cell; cancer; vascular disease; inflammatory disease; inflammatory disease; inflectious disease; human immunodeficiency virus; HIV; immunoglobulin; beta-galactosidase; variable fragment; Fv;
                                                                                                                                                                         DNA encoding anti beta-galactosidase single chain Fv fragment
 747
rrceecesaecaaccaaecreaccerceraeer
                                                                            ABK43226 standard; DNA; 816
                                                                                                                                            (first entry)
                                                                                                                                        05-JUN-2002
715
                                                                                                         ABK43226;
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Unidentified

gene;

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The invention describes a modified virus comprising non-native polypeptides which has framework moieties each containing binding polypeptides which has altered tropism conferrated by the binding moieties. The polypeptides can be expressed in the cytoplasm and nucleus of mammalian host cell in conformation which is maintained in absence of ligands for the binding moieties, where the conformation allows the binding moiety subsequently to bind with the ligand. The modified virus is useful in therapy for the preparation of a medicament for treating tummour cells, cancer, proliferating cells, vascular diseases. Inflammatory diseases and infectious diseases such as Human immunodeficiency virus (HIV). The altered tropisms allow the virus to be used in treatment of disease in human or animal subjects, either by in convoiring treatment. The problems associated with the expression of functional non-native viral components in the nucleus and cytosol of host cells is solved by using the modified virus for the purpose. This fragment (FV) used in the creation of the modified virus containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGGCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                              Novel modified virus comprising non-native polypeptides with stable conformation and having framework moieties containing binding moieties which confer upon the virus, an altered tropism, useful in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGTCTGCCCCGACTCAGCCTCCCTCTGTGTGTGGGTCTCCTGGACAGTCGGTCACCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTGATCGCTTCTCTCGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 816 BP; 181 A; 220 C; 238 G; 177 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33;
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Pred. No. 8e-78
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                      Example 10; Page 148; 163pp; English
                                                                                                                                                                                                            Boulanger PA;
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90.1%;
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                                                                                                                                                                                                            Lindholm L, Nord AK,
                                                                                                                                                                                                                                           WPI; 2002-217049/27
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tes 300; Conserv
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CACCCAGGCAAAGCCCCCCAAACTCATCATTATGAGGTCAGTAATCGGCCCTCAGGGGTT 235
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17-APR-2001; 2001WO-JP03288.
12-SEP-2001; 2001JP-0277314.
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2000JP-0321822.
                                                                                                                                                                                                                                                                                                                                                    20-DEC-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders and cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-OCT-2000;
20-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                     ABX00205;
   176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a new isolated nucleic acid termed ovarian specific nucleic acid (OSNA) comprising: (a) a nucleic acid molecule that encodes any of 53 fully defined protein sequences appearing as ABM51019 -ABM51010 (termed ovarian specific proteins, OSP); (b) any of 76 fully defined nucleotide sequences appearing as ABM52187-ABM52262; or (c) a sequence having at least 60% sequence identity to the nucleic acid molecule of (a) or (b). Also included are a method for determining the presence of an ovary specific nucleic acid (OSNA) in a sample, a vector comprising an OSNA, a host cell comprising the vector.

In a method for determining the presence of an ovary specific protein in a sample and a vaccine comprising an OSP or OSNA. The methods and compositions of the present invention are useful for identifying, diagnosing, monitoring, steaging, imaging and treating ovarian cancer and non-cancerous disease in ovary tissue. The present sequence is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 TCCTGCACTGGAACCAGCAGTCACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                      Human, gene, 88; ovarian specific nucleic acid; OSNA; ovarian cancer; non-cancerous ovarian disease; gene therapy; vaccine; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated OSNA nucleic acid and encoded polypeptide, useful for identifying, diagnosing, monitoring, staging, imaging and treating ovarian cancer and non-cancerous diseases in ovarian tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cafferkey R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1460 BP; 351 A; 466 C; 401 G; 241 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Karra K,
                                                                                                                                                    Human ovarian specific nucleic acid DEX0310_8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1e-76;
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89.5%; Pred. No. 1c
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recipon H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 146; 224pp; English.
                                                       ABX92194 standard; cDNA; 1460 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hu P,
                                                                                                                                                                                                                                                                                                                                                         13-FEB-2002; 2002WO-US22271.
                                                                                                                                                                                                                                                                                                                                                                                       13-FEB-2001; 2001US-268290P.
15-FEB-2001; 2001US-268834P.
                                                                                                                      (first entry)
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Matches 298; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macina RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OSNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (DIAD-) DIADEXUS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-120677/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; ABU61023
                                                                                                                                                                                                                        gynaecological
                                                                                                                                                                                                                                                                                        WO200292785-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C;
                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                      08-MAY-2003
                                                                                                                                                                                                                                                                                                                         21-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salceda S,
                                                                                       ABX92194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
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                                       ABX92194
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CACCCAGGAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGGGGCCTCAGGGGTC

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The invention relates to a new modified single chain Fv antibody
containing at least two Heavy chain variable domains and at least two
light chain variable domains from the same or different monoclonal
antibodies and which is an agonie for crosslinking a molecule at the
cell surface or within the cell and thereby transducing a signal into the
cell. Also include are the DNA encoding the antibody, animal cells and
microorganisms transformed by and expressing the DNA; the preparation of
the antibodies by culture of the transformed cells, drug compositions
containing the antibodies and an assay method for the agonist activity
of the antibodies by contacting the antibodies with cells expressing the
relevant cell surface or internal molecule. The antibodies are useful for
treatment and prevention of cancer, inflammatcory disease, hormonal
disorders including diabetes, autoimmune disease, leukaemia,
disorderinism and blood disorders. The present sequence is a DNA
sequence encoding an antibody of the invention or a fragment thereof.
                                    295
                                                                        241 CAGGCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTA 300
                                                                                            ds; gene; monoclonal antibody; signal transduction agonist; cancer; inflammatory disease; dysendocrinism; blood disease; leukaemia; cytostatic; antiinflammatory; immunosuppressive; immunostimulant;
TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGGCTC
                                    renalicierrenegenceaagrenegeaacacacercecreaceatereageere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified single chain multimeric Fv antibody acting as a signal transduction agonist for treatment of inflammatory hormonal and blood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hormonal disorder; diabetes; autoimmune disease
                                                                                                                                                      333
                                                                                                                                                                              TCGGAACTGGGACCAAGGTCACCGTCCTAGGT 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohtomo T,
                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding single chain antibody 12E10 Fv.
                                                                                                                                                        TTCGGAAGAGGACCCGGTTGACCGTCCTAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 8; Page 208-210; 217pp; Japanese.
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608 AAICGCIICTICIGGCICCAAGICTGGCAACACGGCCTCCCTGACCAICTCTGGGCTCCAG 667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gergaggacgaggergarrarracrgcagercararacaaccagaaggacrccggrgrrc 727
           antibody, and exhibits thrombopoietin (TPO) agonistic effect by causing the TPO receptor to crosslink. The antibodies are useful in preventives and/or remedies for platelet reduction-associated blood diseases, thrombocypoenia following cancer chemotherapy or leukaemia. The antibody can act as a TPO signal transduction agonist by transducing a signal into cells by crosslinking a TPO receptor to exert TPO agonism. This sequence encodes a thrombopoietin (TPO) agonist antibody associated
                                                                                                                                                                                                                                                                                                                                                                            TGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC
                                                                                                                                                                                                                                                                                                                                                                                                            recarregaaccaecaereacerrecrestrataacrarercrestrecracaecae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAAGCGGGCCTCAGGGGTCTCT
chain variable domains and 2 or more light chain variable domains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ds; gene; monoclonal antibody; signal transduction agonist; cancer; inflammatory disease; deuke cytostatic; antiinflammatory; immunosuppressive; immunostimulant; hormonal disorder; diabetes; autoimmune disease.
                                                                                                                                                                                                                          DB 24; Length 792;
                                                                                                                                                                                                                                                             Indela
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                                                                                                                                                                                    C; 217 G; 174 T; 0 other;
                                                                                                                                                                                                                      Score 276.8; DB 24;
Pred. No. 9.2e-77;
0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding single chain antibody sc12E10 Fv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331
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2001WO-JP01912.
2001WO-JP03288.
2001JP-0277314.
                                                                                                                                                                                                                          83.1%;
                                                                                                                                                                                      Sequence 792 BP; 170 A; 231
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                                                                                                                                                                                                                                            Best Local Similarity
Matches 296; Conserv
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20-OCT-2000;
12-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                       GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 243
                                                                                                                                                                                                                                                                                                                                                                            AATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified antibody; thrombopoietin; TPO; agonist;
TPO receptor; platelet reduction-associated blood disease;
thrombocytopenia; cancer chemotherapy; leukaemia; signal transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Degraded thrombopoietin agonist antibodies containing H and L chain V domains of monoclonal antibody, useful in preventives and/or remedies for blood diseases, thrombocytopenia following cancer chemotherapy or
                                                                                                                                                                                                                                                               CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAAGCGGGCCTCAGGGGTCTCT
                                                                                                              4 TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC
                                                                             Gaps
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                                  Score 276.8; DB 24; Length 792; pred. No. 9.2e-77; 0; Mismatches 32; Indels 0;
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 C; 217 G; 174 T; 0 other;
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                                  83.1%;
nilarity 90.2%;
Conservative 0
BP; 170 A; 231
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12-SEP-2001; 2001JP-0277314
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                                                    al Similarity
296; Conserv
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 Sequence 792
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                                                                                                                                                                                                                                        The invention relates to a new modified single chain Fv antibody
containing at least two Heavy chain variable domains and at least two
Light chain variable domains from the same or different monoclonal
antibodies and which is an agonist for crosslinking a molecule at the
cell surface or within the cell and thereby transducing a signal into the
cell surface or within the cell and thereby transducing a signal into the
cell surface or within the cell and thereby transducing a signal into the
microorganisms transformed by and expressing the preparation of
the antibodies by culture of the transformed cells, drug compositions
containing the antibodies and an assay method for the agonist activity
of the antibodies by contacting the antibodies with cells expressing the
relevant cell surface or internal molecule. The antibodies are useful for
treatment and prevention of cancer, inflammatory disease, hormonal
disorders including diabetes, autoimmune disease, leukaemia,
dysendocrinism and blood disorders. The present sequence is a DNA
sequence encoding an antibody of the invention or a fragment thereof.
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                                                                                                Modified single chain multimeric Fv antibody acting as a signal transduction agonist for treatment of inflammatory hormonal and blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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90.2%; Pred. No. 9.3e-77;
ive 0; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 822 BP; 169 A; 233 C; 235 G; 185 T; 0 other;
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Matches 296; Conservative
                                                                                                                                               disorders and cancer
                       WPI; 2002-682599/73.
P-PSDB; ABG97835.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes a modified antibody comprising at least 2 heavy chain variable domains and 2 or more light chain variable domains of an antibody, and exhibits thrombopoietin (TPO) agonistic effect by causing the TPO receptor to crosslink. The antibodies are useful in preventives and/or remedies for platelet reduction-associated blood diseases, thrombocytopenia following cancer chemotherapy or leukaemia. The antibody can act as a TPO signal transduction agonist by transducing a signal into cells by crosslinking a TPO receptor to exert TPO agonism. This sequence encodes a thrombopoietin (TPO) agonist antibody associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
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                                                                                                                                                                                                                                20-OCT-2000; 2000JP-0321821.
17-APR-2001; 2001WO-JP03288.
12-SEP-2001; 2001JP-0277314.
                                                                                                                      22-OCT-2001; 2001WO-JP09259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHUS ) CHUGAI SEIYAKU KK
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25-APR-2002
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completed: December 29, 2003, 16:25:34 ne : 146.29 secs

time Search Job tim

Modified antibody; thrombopoietin; TPO; agonist; TPO receptor; platelet reduction-associated blood disease; thrombocytopenia; cancer chemotherapy; leukaemia; signal transduction;

Synthetic

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Sequence 1 Sequence 1

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Sequence Sequence

Sequence 970,

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Run on:

Sequence:

Minimum DB 8 Maximum DB 8

Database

Result Š.

Searched:

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TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE THEREOF AS THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZID: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
STREET: P.O. Box 1404
US-10-039-785-54
US-09-974-49-7
US-10-139-785-57
US-10-139-785-60
US-10-139-785-60
US-10-139-785-60
US-10-139-785-60
US-10-139-785-16500
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APPLICATION NUMBER: US/09/019,441
FILING DATE: 05-Feb-1998
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
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Publication No. US20030086921A1
GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
KLOETZER, William S.
NAKAWURA, Takehiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (703) 836-6620
703) 836-2021
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INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                   December 29, 2003, 19:01:43; Search time 481.099 Seconds (without alignments) 2371.523 Million cell updates/sec
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Sequence 8
Sequence 3
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                         GenCore version 5.1.6
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US-10-10-686-1

US-10-151-882-4

US-10-139-785-63

US-10-139-785-64

US-10-139-785-64

US-10-039-785-64

US-10-039-785-64

US-10-039-785-64

US-10-039-785-64

US-10-198-846-13540

US-10-198-846-13540

US-10-198-846-13506

US-10-199-846-13206

US-10-139-846-13206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published_Applications_NA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                    nucleic search, using sw model
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                                                                                                                                                                                                                                                                                          IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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length: 2000000000
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Perfect score:
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Publication No. US20030059862A1
GENERAL INFORMATION:
APPLICAUT: Ruben, Steven M.
TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
CURRENT APPLICATION NUMBER: US/10/151,882
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR PILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 48
SSOTHARE: Patentin version 3.0
SSOTHARE: Patentin version 3.0
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100.0%; Pred. No. 7.2e-102;
tive 0; Mismatches 0;
           ATTORNEY AGENT INPORMATION:
NAME: Teskin, Robin L.
REGISTATION UNBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 836-620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 333
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ORGANISM: Artificial Sequence
FARTURE:
OTHER INFORMATION: DNA encoding A027A11 scFv
                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 58.7390
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                      mat_peptide
58..390
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LOCATION:
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NAME/KEY:
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Publication No. US20030059424A1
GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
KLOETZER, William S.
NAKAMURA, Takehiko
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
ANTIBODIES AND USE THEREOF AS THERAPEUTICS
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CORRESPONDENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404

CITY: Alexandria
STATE: Viginia
COUNTY: United States
ZIP: 22313-1404

COMPUTER READABLE FORM:
WEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION: CURNOWN>
                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 333; DB 11; Best Local Similarity 100.0%; Pred. No. 7.2e-102; Matches 333; Conservative 0; Mismatches 0;
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APPLICATION NUMBER: US/08/803,085
                                                                                                                                                                                                              NAME/KEY: mat_peptide
LOCATION: 58.7390
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                   LENGTH: 390 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                        1..390
                                                                                                                                                                        LOCATION:
                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                            FEATURE:
                                                                                                                              FEATURE:
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US-10-103-686-1
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GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REPERENCE: PF50
CURRENT APPLICATION NUMBER: US/10/139,785
CURRENT FILING DATE: 2002-05-07
PRIOR FILING DATE: 2002-05-07
PRIOR FILING DATE: 2001-12-20
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR PLING DATE: 2001-08-02
PRIOR PLING DATE: 2001-08-04
PRIOR FILING DATE: 2001-08-04
PRIOR FILING DATE: 2001-08-05
PRIOR PLING DATE: 2001-08-05
                                                                                                                                                                                                                                                                                        CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC
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                              1 CAGICIGCCCCGACICAGCCICCCCTCTGTGTCTGGGTCT
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Publication No. US20030190685A1
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Matches 302; Conservative
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/139,785
CURRENT APPLICATION NUMBER: 60/341,237
PRIOR PILING DATE: 2002-04-05
PRIOR PILING DATE: 2001-12-20
PRIOR PILING DATE: 2001-11-20
PRIOR PILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR PILING DATE: 2001-09-21
PRIOR PILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
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PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-07
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                                                          Length 726;
                                                          Score 283.4; DB 15; Length
Pred. No. 4.7e-85;
0; Mismatches 31; Indels
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llarity 90.7%;
Conservative
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ORGANISM: Artificial sequence
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Best Local Similarity 90.7
Matches 302; Conservative
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US-10-151-882-4
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CURRENT FILING DATE: 2002-05-05
PRIOR PAPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05
PRIOR FILING DATE: 2001-05-05-05
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-07
PRIOR PRIOR DATE: 2001-10-09
PRIOR FILING DATE: 2001-09-21
PRIOR PILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-06-05
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APPLICANT: Salcedo et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

CURRENT APPLICATION NUMBER: US/10/139,785

CURRENT FILING DATE: 2002-05-07

PRIOR FILING DATE: 2002-04-05

PRIOR APPLICATION NUMBER: 60/331,310

PRIOR APPLICATION NUMBER: 60/331,310

PRIOR FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-00-09

PRIOR FILING DATE: 2001-00-09

PRIOR FILING DATE: 2001-09-21

PRIOR FILING DATE: 2001-09-21

PRIOR PLICATION NUMBER: 60/309,176

PRIOR PLICATION NUMBER: 60/309,176

PRIOR PLING DATE: 2001-09-21

PRIOR PLING DATE: 2001-08-02

PRIOR PLING DATE: 2001-06-04

PRIOR FILING DATE: 2001-06-05

NUMBER OF SEQ ID NOS: 66
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US-10-139-785-64
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; Sequence 64, Application US/10139785
; Publication No. US20030190685A1
; GENERAL INFORMATION:
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85.1%; Score 283.4; DB 14; Length 735;
Best Local Similarity 90.7%; Pred. No. 4.7e-85;
Matches 302; Conservative 0; Mismatches 31; Indels 0;
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; OTHER INFORMATION: DNA encoding T1015E01 scFv
US-10-039-785-64
                                                                                               703 TTCGGCGGAGGACCAAGGTCACCGTCCTAGGT
                                          TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT
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PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/309,176
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                      Sequence 64, Application US/10039785
Publication No. US20020067646A1
GENERAL INFORMATION:
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT APPLICATION NUMBER: US/2002-05-07
PRIOR PILING DATE: 2002-05-07
PRIOR FILING DATE: 2002-04-05
PRIOR FILING DATE: 2001-12-20
PRIOR PLICATION NUMBER: 60/331,310
PRIOR PLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-04
PRIOR FILING DATE: 2001-11-05
PRIOR FILING DATE: 2001-0-09-07
PRIOR FILING DATE: 2001-0-09-07
PRIOR PLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-06-04
PRIOR PLICATION NUMBER: 60/309,176
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; OTHER INFORMATION: DNA encoding T1015A07 scFv
US-10-039-785-63
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ORGANISM: Artificial sequence
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                                                                                                                                                                                                                                                                                                                                                                        Length 1460;
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; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyesq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBT
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REPERBNCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/235,076
; PRIOR RILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                      Score 277; DB 13;
Pred. No. 8.8e-83;
0; Mismatches 35;
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0; Mismatches 36
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89.2%; Pred. No. 1.90
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 36573
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION UNMBER: 60/268,834
PRIOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Patentin version 3.1
SEQ ID NO ELENGTH: 1460
                                                                                                                                                                                                                                                                                                                                                                        83.2%;
                                                                                                                                                                                                                                                NAME/KEY: misc_feature
| LOCATION: (1022) .. (1022)
| OTHER INFORMATION: a, c, g or
US-10-076-747-8
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 89.59
Matches 298; Conservative
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Best Local Similarity 89.2
Matches 297; Conservative
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US-09-918-995-36573
                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-918-995-36573
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                                                                                                                                                                                                                              FEATURE:
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Publication No. US20030180726A1
GENERAL INFORMATION
APPLICANT: Salceda, Susana
APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Hu, Ping
APPLICANT: Karra, Kalpana
APPLICANT: San, Yoongming
APPLICANT: Sun, Yoongming
APPLICANT: Sun, Yoongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Ovarian Specific Genes and FILE REFERENCE: DEX-0315
CURRENT APPLICATION NUMBER: US/10/076,747
CURRENT PILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: 60/268,290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1473 CÁGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATC 1414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1413 TCCTGCATTGGAACCTTCAATGACATTGGTAGTTATAACTATGTTTCCTGGTTCCAACAA 1354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACCCAGGCAAAGCCCCCCAAACTCCTGATTTATGATGTCAGTAATCGGCCCTCAGGGGTT 1294
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                                                                  Sequence 13540, Application US/10198846

Publication No. US2003009974A1

GENERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: Lillie, James

APPLICANT: Lillie, James

APPLICANT: Wang, Youzhen

APPLICANT: Steinmann, Kathleen

APPLICANT: Steinmann, Kathleen

APPLICANT: Steinmann, Kathleen

APPLICANT: Wang, Youzhen

APPLICANT: Wang, Youzhen

APPLICANT: Wang, Youzhen

APPLICANT: Steinmann, Kathleen

APPLICANT: Wang, Youzhen

APPLICANT: Steinmann, Wathleen

APPLICANT: Steinmann, Wathleen

FILLE OF INVENTION: THERAPY OF BREAST CANCER

FILLE REFERENCE: MRI-049

CURRENT APPLICATION NUMBER: 05/10/198,846

CURRENT PILING DATE: 2001-07-18

PRIOR FILING DATE: 2001-07-18

NUMBER OF SEQ ID NOS: 14084

SOFTWARE FREESEQ for Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CAGICTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATC
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Pred. No. 7.6e-84;
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90.1%;
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Best Local Similarity 90.1
Matches 300; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapiens
US-10-198-846-13540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 13540
LENGTH: 1597
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; ORGANISM: Homo
US-10-198-846-13206
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                       TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 120
                                                                  CACCCAGGCAAAGCCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC 180
                                                                                                     255
                                                                                                                                     TCTGATCGCTTCTCTCGCCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 240
                                                                                                                                                                                                        CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTGTTA 300
                                                                                                                                                                                                                                          CAGGCTGAGGACGAGGCTCATTATTACAGTTCATATACAACCAGAAGCACTCTCGTC 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 120
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                                                                                      CACCCAGGCAAAGCCCCCAAACTCATAATTTATGAGGTCAGTAATCGGCCCTCAGGGGTT
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 2011-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01.20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 275.4; DB 11; Length
Pred. No. 1.9e-82;
0; Mismatches 36; Indels
                                                                                                                                                                                                                                                                            TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 333
                                                                                                                                                                                                                                                                                                           rrcegaaareeeccaaeercaccercrarer 408
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89.2%;
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Best Local Similarity 89.2
Matches 297; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                   US-09-918-995-16692
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US-09-918-995-16692
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RESULT 14 US-10-198-846-13206/c

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Publication No. US20030190685A1

GRNERAL INFORMATION:
APPLICANT SAlcedo et al.
TITLE OF INVENTION: Receptors
TITLE OF INVENTION: Receptors
FILIS REFERENCE: PF550

CURRENT APPLICATION NUMBER: US/10/139,785

CURRENT FILING DATE: 2002-05-07

PRIOR FILING DATE: 2001-05-07

PRIOR PILING DATE: 2001-11-20

PRIOR PELION NUMBER: 60/341,237

PRIOR PILING DATE: 2001-11-20

FRIOR PELION NUMBER: 60/331,310

PRIOR PILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-11-14

PRIOR PLING DATE: 2001-11-14

PRIOR PLING DATE: 2001-11-07

PRIOR PLING DATE: 2001-11-07

PRIOR PLING DATE: 2001-11-07

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                                                                                                                                                                                                                                               AND METHODS
PREVENTION, AND
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                                                                                                                             APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: VOYEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: POR IDENTIFICATION, ASSESSMENT, PRE;
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: RMI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR PILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 333
Sequence 13206, Application US/10198846
Publication No. US20030099974A1
                                    Publication No. US2003009999999999 GENERAL INFORMATION:
APPLICANT: Lillie, James
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61 TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 120
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82.2%; Score 273.8; DB 13; Length 735;
Best Local Similarity 88.9%; Pred. No. 8.2e-82;
Matches 296; Conservative 0; Mismatches 37; Indels 0;
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                                                                                                                                                                                                                                                                        TYPE: DNA PATIFICIAL SEQUENCE PEATURE: PEATURE: PEATURE: NOTER INFORMATION: DNA encoding T1014A04 scFv US-10-139-785-54
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PRIOR APPLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21
PRIOR PELING DATE: 2001-09-01
PRIOR PILING DATE: 2001-08-02
PRIOR PILING DATE: 2001-06-04
PRIOR PILING DATE: 2001-06-04
PRIOR PILING DATE: 2001-06-34
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PALENTIN VET: 2.1
SEQ ID NO 54
LENGTH: 735
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Sequence 9, Appli Sequence 4, Appli Sequence 133, Appl Sequence 133, Appl Sequence 13, Appl Sequence 43, Appl Sequence 63, Appl Sequence 63, Appl Sequence 63, Appl

Sequence Sequence Sequence

Sequence Sequence Sequence 3

Sequence

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Run on:

Sequence:

Searched:

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Squence 1, Application US/08803085

Patent No. 601138

GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
APPLICANT: KLOETZER, William S.
APPLICANT: MAKAMUBA, Takehiko
TITLE OF INVENTION: GAWMA-1 ANTI-HUMAN CD23 MONOCLONAL
TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FEB-1997
CLASSIFICATION: A24
ATTORNEY/ACENT INFORMATION:
NAME: Teskin, Robin I.
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
REFERENCE/TOXIN 1876-6620
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-8620
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
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US-10-039-785-56
US-09-273-839A-9
US-09-240-274-126
                                                                                                             US-09-240-274-133
US-09-240-274-132
US-08-199-911-1
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CITY: Alexandria STATE: Viginia
COUNTRY: United States
ZIP: 22313-1404
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LOCATION:
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LOCATION:
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December 29, 2003, 16:08:50 ; Search time 36.6551 Seconds (without alignments) 4009.823 Million cell updates/sec
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.: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
.: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
.: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
.: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
.: /cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
.: /cgn2_6/ptodata/2/ina/pcTuS_COMB.seq:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-958-201-11
US-08-958-201-11
US-10-039-785-54
US-09-049-672A-23
US-08-378-939-11
US-10-039-785-60
US-10-039-785-61
US-10-039-785-61
US-10-039-785-61
US-10-039-785-61
US-10-039-785-61
US-10-039-785-61
US-10-039-785-61
US-09-736-45705-970
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                                                                                                                                                                                                                                                                                                    569978 seqs, 220691566 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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Sequence 59, Application US/10039785
Patent No. 6538938
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-04-05
PRIOR PILING DATE: 2002-04-06
PRIOR PILING DATE: 2001-12-20
PRIOR PILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-09
PRIOR PLICATION NUMBER: 60/331,344
PRIOR FILING DATE: 2001-10-09
PRIOR PLICATION NUMBER: 60/323,807
PRIOR PLICATION NUMBER: 60/323,807
PRIOR PLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21
PRIOR PLICATION NUMBER: 60/323,473
PRIOR PLICATION NUMBER: 60/294,981
PRIOR PLICATION NUMBER: 60/294,981
PRIOR PLICATION NUMBER: 60/294,981
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                         Indels
100.0%; Pred. No. 2.2e-95; tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 333; Conservative
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APPLICANT: Salcede et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Receptors
FILE REFERENCE: PF550

CURRENT FILING DATE: 2002-06-07

PRIOR PILING DATE: 2002-04-05

PRIOR PLICATION NUMBER: 60/331,310

PRIOR PILING DATE: 2001-12-20

PRIOR PLICATION NUMBER: 60/331,310

PRIOR PLICATION NUMBER: 60/331,044

PRIOR PLICATION NUMBER: 60/331,044

PRIOR PLICATION NUMBER: 60/331,044

PRIOR PLICATION NUMBER: 60/323,807

PRIOR PLICATION NUMBER: 60/323,807

PRIOR PLICATION NUMBER: 60/323,407

PRIOR PLICATION NUMBER: 60/329,473

PRIOR PLICATION NUMBER: 60/329,473

PRIOR PLICATION NUMBER: 60/229,473

PRIOR PLICATION NUMBER: 60/299,981

PRIOR PLICATION NUMBER: 60/299,491

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US-10-039-785-63
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Best Local Similarity 90.7
Matches 302; Conservative
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Pred. No. 2.6e-77;
0; Mismatches 36;
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APPLICATION NUMBER: US 60/028,897
FILING DATE: 21-0CT-1996
INFORMATION FOR SEQ 1D NO: 13:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/08/958,201
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/08958201
Patent No. 5977319
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Pope, Anthony R
APPLICANT: Pritchard, Kevin
APPLICANT: Williams, Andrew J
APPLICANT: Williams, Andrew J
APPLICANT: Johnson, Kevin S
TITLE OF INVENTION: Specific bir
TITLE OF INVENTION: materials an NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Ge
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Best Local Similarity 89.2
Matches 297; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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STRANDEDNESS: double
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US-08-958-201-13
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
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Pred. No. 1.1e-79;
0; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TICGGAAGAGGACCCGGTTGACCGTCCTAGGT 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
; OTHER INFORMATION: DNA encoding T1015E01 scFv
US-10-039-785-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: PF520

CURRENT PELING DATE: 2002-05-07

PRIOR APPLICATION NUMBER: 60/369,860

PRIOR FILING DATE: 2002-06-07

PRIOR FILING DATE: 2001-04-05

PRIOR FILING DATE: 2001-12-20

PRIOR FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR PELING DATE: 2001-11-07

PRIOR APPLICATION NUMBER: 60/331,044

PRIOR FILING DATE: 2001-11-07

PRIOR APPLICATION NUMBER: 60/321,864

PRIOR FILING DATE: 2001-10-09

PRIOR FILING DATE: 2001-10-09

PRIOR FILING DATE: 2001-09-21

PRIOR FILING DATE: 2001-09-21

PRIOR FILING DATE: 2001-06-04

PRIOR FILING DATE: 2001-06-04

PRIOR FILING DATE: 2001-06-04

PRIOR APPLICATION NUMBER: 60/294,981

PRIOR FILING DATE: 2001-06-04

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Patent No. 6538938
GENERAL INFORMATION:
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ORGANISM: Artificial sequence
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Best Local Similarity 90.7%;
Matches 302; Conservative
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APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Acceptors
FILE OF INVENTION: Receptors
FILE OF INVENTION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-14
PRIOR PELING DATE: 2001-11-14
PRIOR PELING DATE: 2001-11-17
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Pred. No. 1.1e-76;
0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                        TTCGGAAGAGGGACCCGTTGACCGTCCTAGGT 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: DNA encoding T1014A04 scFv
US-10-039-785-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 54, Application US/10039785
Patent No. 6538938
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ORGANISM: Artificial sequence
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Best Local Similarity 88.99
Matches 296; Conservative
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Patent No. 5977319

GENERAL INFORMATION:
APPLICANT: Pritchard, Kevin
APPLICANT: Williams, Andrew J
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTINE: IBM PC COMPUTINE:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.25 (EPO)
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: 6300 Sears Tower, 233 South Wacker Drive
Chicago
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Pred. No. 8.4e-77;
0; Mismatches 37
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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CLONE: D12 (light chain)
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Best Local Similarity 88.9
Matches 296; Conservative
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CITY: CP
STATE: 1
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241 CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTA 300
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    TCCCCAGGCACGCCCCCCAAACTCATGATTTATGAGGTCAGTAATCGGCCCTCAGGGGTT 270

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
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                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/08378939
Patent No. 5876961
GENERAL INFORMATION:
APPLICANT: LEWIS, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVARINO: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 272.2;
Pred. No. 3.8e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERNST & KURZ
                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: SCHWELL, FIGG, ERNST CITY: WASHINGTON STATE: D. C. COUNTRY: IT C. ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808
TELECOMMUNICATION INFORMATION:
TELEPAX: (202) 783-6040
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 902 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
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Best Local Similarity 88.6%;
Matches 295; Conservative
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TYPE: nucleic acid
STRANDEDNESS: both
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                       181 TCTGATCGCTTC
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LOCATION:
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LOCATION:
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FEATURE:
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; LOCATION:
US-08-378-939-11
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                                                                                                                                                                                                                                                                             APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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88.9%; Pred. No. 1.2e-76;
                       TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 333
                                                         703 Treegegagaccaagergaccircraggr 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
CUNTARE: FastsED for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA
                                                                                                                                                 Sequence 23, Application US/09049672A
Patent No. 6155941
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/OCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTR.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 891 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.9
Matches 296; Conservative
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Tang, Y. Tom
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Tang, r
Henry
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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; CLONE: 2872705
US-09-049-672A-23
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                                                                                                                                   US-09-049-672A-23
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APPLICANT:
                       301
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; OTHER INFORMATION: DNA encoding T1014F08 scFv US-10-039-785-60
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Patent No. 6538938
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                                                                                                                                  CACCCAGGCAAAGCCCCCCAAACTCATGATGTTGTCGCTAAGCGGGCCTCAGGGGTC 180
                                                                                                                                                                                                                                             CAGGCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTGTTA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE NEFERENCE: PF550
CURRENT FILING DATE: 2002-05-07
PRIOR PELICATION NUMBER: 60/369,860
PRIOR PELICATION NUMBER: 60/341,237
PRIOR PELICATION NUMBER: 60/331,310
PRIOR PELICATION NUMBER: 60/331,310
PRIOR PILING DATE: 2001-11-14
PRIOR PELICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-14
PRIOR PELICATION NUMBER: 60/331,044
PRIOR PILING DATE: 2001-11-0-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-00-01
PRIOR PILING DATE: 2001-00-01
PRIOR PILING DATE: 2001-00-01
PRIOR PILING DATE: 2001-00-02
PRIOR PILING DATE: 2001-00-02
PRIOR PILING DATE: 2001-00-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 TTCGGAAGAGGACCCGGTTGACCGTCCTAGGT 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , OTHER INFORMATION: DNA encoding T1014A12 scFv
US-10-039-785-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 57, Application US/10039785
Patent No. 6538938
GENERAL INFORMATION:
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APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF550
CURRENT PAPLICATION NUMBER: US/10/039,785
CURRENT PAPLICATION NUMBER: 60/349,860
PRIOR PAPLICATION NUMBER: 60/341,237
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-04
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Salcedo et al. TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL TITLE OF INVENTION: Receptors FILE REFERENCE: PFSSO.
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77.9%; Score 259.4; DB 4
Best Local Similarity 86.2%; Pred. No. 3.7e-72;
Matches 287; Conservative 0; Mismatches 46
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US-10-039-785-61
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CURRENT APPLICATION NUMBER: US/10/039,785

CURRENT FILING DATE: 2002-05-07

PRIOR APPLICATION NUMBER: 60/341,237

PRIOR PLILNG DATE: 2001-04-05

PRIOR PLILNG DATE: 2001-12-20

PRIOR APPLICATION NUMBER: 60/331,310

PRIOR FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-11-07

PRIOR PLILNG DATE: 2001-11-07

PRIOR APPLICATION NUMBER: 60/331,044

PRIOR PLILNG DATE: 2001-11-07

PRIOR APPLICATION NUMBER: 60/327,364

PRIOR PLING DATE: 2001-10-09

PRIOR PLING DATE: 2001-09-21

PRIOR PLING DATE: 2001-09-21

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PRIOR PLING DATE: 2001-09-21

PRIOR PLING DATE: 2001-09-21

PRIOR PLING DATE: 2001-09-21

PRIOR PLING DATE: 2001-06-04

PRIOR PLING DATE: 2001-06-04

PRIOR PLING DATE: 2001-06-04
                                                             241 CAGGCTGAGGACGAGGCTGATTATTACT
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Patent No. 6538938
GENERAL INFORMATION:
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SOFWARE: PatentIn Ver. 2.1
SEQ ID NO 61
LENGTH: 735
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J. GENERAL INCORMATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Receptors

FILE REPERENCE: PF550

CURRENT FILING DATE: 2002-04-07

PRIOR PELICATION NUMBER: 60/341,237

PRIOR PELICATION NUMBER: 60/331,310

PRIOR PELICATION NUMBER: 60/331,310

PRIOR FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-11-14

PRIOR PELICATION NUMBER: 60/331,044

PRIOR FILING DATE: 2001-11-04

PRIOR FILING DATE: 2001-10-09

PRIOR FILING DATE: 2001-10-09-21

PRIOR FILING DATE: 2001-09-21

PRIOR PELICATION NUMBER: 60/294,981

PRIOR PELICATION NUMBER: 60/293,473

PRIOR PELING DATE: 2001-06-04

PRIOR PELING DATE: 2001-06-04

PRIOR APPLICATION NUMBER: 60/293,473

PRIOR PILING DATE: 2001-06-04

PRIOR PELING DATE: 2001-06-05

PRIOR PELING DATE: 2001-06-05

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; OTHER INFORMATION: DNA encoding T1014B01 scFv
US-10-039-785-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 58, Application US/10039785
Patent No. 6538938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial sequence
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Best Local Similarity 86.2
Matches 287; Conservative
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US-10-039-785-58
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                                                                                                                                                                                             APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Marc
APPLICANT: Retter, Marc
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT APPLICATION NUMBER: US/09/702,705
SOFTWARE: FastSEQ for Windows Version 3.0
SSD ID NO 970
LENGTH: 543
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                                  Sequence 970, Application US/09702705 Patent No. 6504010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.7%;
92.0%;
                                                                                                         Wang, Tongtong
Bangur, Chaitanya
Lodes, Michael A.
                                                                                                                                                                                Fanger, Gary
Vedvick, Tom
Carter, Darrick
Retter, Marc
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Best Local Similarity 92.0°
Matches 266; Conservative
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US-09-702-705-970
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                                                                                                                                            Sequence 55. Application US/10039785
; Sequence 55. Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: 60/369,860
} RIOR APPLICATION NUMBER: 60/341,237
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
; PRIOR FILING DATE: 2001-10-09
; PRIOR FILING DATE: 2001-10-09
; PRIOR FILING DATE: 2001-10-09
; PRIOR PELING DATE: 2001-00-921
; PRIOR PILING DATE: 2001-00-921
; PRIOR FILING DATE: 2001-00-921
; PRIOR FILING DATE: 2001-00-921
; PRIOR FILING DATE: 2001-08-02
; PRIOR PILING DATE: 2001-08-02
; PRIOR FILING DATE: 2001-08-02
; PRIOR FILING DATE: 2001-06-04
; PRIOR FILING DATE: 2001-06-04
; PRIOR FILING DATE: 2001-06-04
; PRIOR PILING DATE: 2001-06-04
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333
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                                         703 rrcegecegaegeaccaaegercaccerceraegr 735
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US-10-039-785-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial sequence
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SOFTWARE: Patentin Ver.
                                                                                                                                       US-10-039-785-55
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LENGTH: 735
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Indels

Score 252.2; DB 4; Pred. No. 6.1e-70; 0; Mismatches 23;

Length 543;

484

224 364

OM nucleic - nucleic search, using sw model Run on:

December 29, 2003, 16:08:50 ; Search time 1516.15 Seconds (without alignments) 9875.644 Million cell updates/sec

US-09-019-441-2\_COPY\_58\_423 366 1 CAGCTGCAGCTGCAGGAGTC.....TCCTGGTCACCGTCTCCTCA 366

Title: Perfect score: Sequence:

2888711 seqs, 20454813386 residues Searched:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

Scoring table:

5777422 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:\* Database

gb\_ba: \*
gb\_ntg: \*
gb\_ntg: \*
gb\_on: \*
gb\_pt: \*
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em\_hum:\* em\_in:\* em\_mu:\* em\_om:\* em\_or:\* em\_ov:\* em\_pat:\*

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em\_htgo\_mus:\* em\_htgo\_other:\* em\_htg\_rod: \*
em\_htg\_mam: \*
em\_htg\_vrt: \* em\_htgo\_hum:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		416358 Pap	7559 Macaca	16359 Papic	79514 Homo	179 Human i	560 Macaca	3307 Macaca	558 Macaca	7952	Human i	565 Macaca	7563 Macaca	45032 Homo	910 H.sapi	7568 Macaca	79522 Homo	120 Homo	<b>H</b>	367 Sequ	AR265201 Sequence	39 Identifi	946 Homo sa	549 Homo sap	7 H.sapi	Hum 1	899 Syn	Hum 2	5 H	~	583 M	176	ě	584	É	399 H.sapiens	586 Macaca m	5015	905 H.sapien	17843	245026 Homo	5364 H.sapie	566 Macaca	197 Human (clo	245023	027 Homo sap	
ID			755	335	795	7	MMU57560	ĸ	MMU57558	795	œ		MMU57563		XX2	MMU57568	S	AF062120	HUMIGHRH	AR108867	AR265201	BD063039	1494		-	HSU80141	AF4528	HUMIGHZF	HSU80125	MMU57582	MMU57583	HSA389176	: AF452934	999	HSU80176	HST22X26	MMU57586	HSA245015	HSIGHXX23	AF417843	HSA245026	HST14X12	MMU57566	HUMIGHVRN	450	02	
gth DB	1		63	41	63	63	20	359	373	99	68	20	11	63	23	14	63	9	20	431	431 6	431	363	63	20	99	03	89	64	99	99	75	12	63	99	14	57	54	14	98	54	23	35	360 9	75	63	}
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Score	1	271.6	270	N	268.4	68	99	99	65	63	~	262	19	9	260.2	59	57	~	56	56	256.2	56	55	55	55	55	N	54	254.2	54	54	~	53	252.4	52	51	251	250	249.6	249	248.4	248	248	47	247.6	47.	
Result No.		-1	7	e	4	w	9	7	00	Ó	10	11	12	13	14	15	19	17	18	61.	200	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	<b>!</b>

ALIGNMENTS

RESULT 1 AF416358 LOCUS DEFINITION

435 bp mRNA linear PRI 27-MAR-2002 Papio cynocephalus anubis clone VH4-4 immunoglobulin heavy chain variable region mRNA, partial cds. AF416358.1 GI:19744277 ACCESSION

VERSION KEYWORDS -SOURCE -

Papio anubis (olive baboon)

Papio anubis Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Papio. 1 (bases 1 to 415) Scinicariello,F., Jayashankar,L. and Attanasio,R.

REFERENCE AUTHORS

Hines

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Papio cynocephalus anubis clone VH4-7 immunoglobulin heavy chain variable region mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="QVQLQESGPGLVKPSETLSLTCAVSGGSISGGFDWGWIRQPPGK
GLEWIGYIYGSSGSTNYNPSLKNRVTISKDTSKNQFSLKLSSVTAADTAVYYCARGSS
                                                      Roubinet, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ACCTGCGCTGTCTCTGGAGGCTCTATCAGCGGTGGTTTTGACTGGGGCTGGATCCGCCAG 120
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                                                                                                                                                                                                                                                                                                                  Blancher, A
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                           Andria, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Roubine Blancher, A. and Capra, J.D.
Blancher, A. and Capra, J.D.
Variable region gene segment utilization in rhesus monkey hybridomas producing human red blood cell-specific antibodies: predominance of the VH4 family but not VH4-21 (V4-34) Mol. Immunol. 34 (3), 237-253 (1997)
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Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Ce.
University of Texas Southwestern Medical Center, 6000 Harry I
Blvd., Dallas, TX 75235-9140, USA
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Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., and Capra,J.D.
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85.5%; Pred. No. 2.3e-67;
tive 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <1. .>363
/codon start=1
/product="immunoglobulin heavy chain"
/protein id="AAC02636.1"
/db_xref="G1:1575066"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Macaca mulatta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9544"
/note="hybridoma"
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101 c 113 g
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      Cercopithecinae; Macaca.
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Matches 313; Conserv
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GGSISSSYWGWIRQAEKGLEWIGGIYSNSGWTYYNPELKNRVTISTDTSKNQPSLKL
SSVTAADTAVYYCARDLGAYNWGPQHYWGQGVLVTVSSASASA"
1 131 c 124 g 92 t
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Macaca mulatta Ig rearranged heavy chain variable region, antl-RBC
antibody, mRNA, partial cds.
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Baboon immunoglobulin variable region heavy chains: identification of genes homologous to members of the human IGHV1-IGHV7 subgroups Immunogenetics 53 (10-11), 815-820 (2002)
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Macaca mulatta
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355 CTTGGGGCTTATAACTGGGGACCACACACTACTGGGGCCCAGGGAGTCCTGGTCACCGTC
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product="immunoglobulin heavy chain variable region"
protein i="AAL96424.1"
/db_xref="G1:19744278"
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                                                                                                                                                2 (bases 1 to 435)
Scinicariello,F., Jayashankar,L. and Attanasio,R.
Direct Submission
Submitted (04-SEP-2001) Department of Biology, Ge
University, PO BOX 4010, Atlanta, GA 30302, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9;
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85.8%; Pred. No. 7.8e-68;
iive 0; Mismatches 49
                                                                                                                                                                                                                                                                                                                                             /organiam="Papio anubis"
/mol_type="mRNA"
shub_specie="anubis"
/db_xref="taxon:9555"
/clone="VH4-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 g
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AUTHORS
TITLE
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Homo sapiens mRNA for immunoglobulin mu heavy chain variable
                                                                                                Homo sapiens (human)
Homo sapiens
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GGSISSGYYWGWIRQPPGKGLEWIGNIDGNSASTNYNPSLKORYTISKDTSKNQFSLK
LSSTTAADTAVYXCARDWTYSGNYKYGLDAWGQGVVVTVSSASAS"
126 c 157 g 95 t
                                                                                                                             Scinicariello, F., Jayashankar, L. and Attanasio, R.
Baboon immunoglobulin variable region heavy chains: identification
of genes homologous to members of the human IGHV1-IGHV7 subgroups
Immunogenetics 53 (10-11), 815-820 (2002)
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                                                Papio anubis
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Papio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="immunoglobulin heavy chain variable region"
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                                                                                                                                                                                                                            2 (bases 1 to 441)
Scinicariello,F., Jayashankar,L. and Attanasio,R.
Direct Submission
Submitted (14-SEP-2011) Department of Biology, Ge
University, PO BOX 4010, Atlanta, GA 30302, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                       /organism="Papio anubis"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9555"
/clone="VH4-7"
                                    anubis (olive baboon)
     AF416359.1 GI:19744279
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                                    Papio
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Matches 316;
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Submitted (11-JAN-2000) Dono M., Istituto Nazionale per la Ricerca
sul Cancro, Immunologia Clinica, L.go Rosanna benzi 10- Genova,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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J. Immunol. 164 (11), 5596-5604 (2000)
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85.2%; Pred. No. 6.6e-67;
iive 0; Mismatches 51;
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region, partial, clone CD27low-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="IgD-low SE
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/producer=immunoglobulin heavy chain"
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GRISLIAADTAVFXADGGYSSRFPDYWGQGVLVTVSS"
a 128 c 121 g 95 t
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Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC
merrody, mRNA, partial cds.
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1 (Dases 1 to 420)
Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Roubinet,F.,
Blancher,A. and Capra,J.D.
Variable region gene segment utilization in rhesus monkey
hybridomas producing human red blood cell-specific antibodies:
predominance of the VH4 family but not VH4-21 (V4-34)
Mol. Immunol. 34 (3), 237-253 (1997)
                                                                                                                                                                            241 TCCCTGAACCTGAACTCTGTGACCGCGGCCGGACACGGCCGTGTATTACTGTGCCAGAGAT 300
                                                                                                                                                                                                 238 TCCCTGAAGCTGAGCTCTGTGACCGCGGGGACACGGCCGTGTATACTGTGCGGAGAGA 297
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                                                    121 cccccadedaadedecredadredarrededaarcrarcara---Gredeadcaccaac 177
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Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.
and Capra, J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (06-NAY-1996) J.S. Andris, Molecular Immunology Center,
University of Southwestern Medical Center, 6000 Harry Hines
Blvd., Dallas, TX 7535-9140, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGCTGCAGCTGCAGGAGTCGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC 60
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                              TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC
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85.0%; Pred. No. 1.9e-66;
tive 0; Mismatches 52;
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/db_xref="taxon:9544"
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                                                                                                                                                                                                                                                          Human immunoglobulin heavy chain variable region (V4-4b) gene, partial cds.
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Direct Submission
Submitted (12-NOV-1996) Immunology, Virginia Mason Research Center,
1000 Seneca Street, Seattle, WA 98101, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /trānslation="QVQLQESGPGLVKPSGTLSLTCAVSGGSISSSNWWSWVRQPPGK
GLEWIGBIYHSGSTNYNPSLKSRVTISVDKSKNQFSLKLSSVTAADTAVYYCARGIPH
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                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 363)

Glas,A.M., Nottenburg,C. and Milner,E.C.

Analysis of rearranged immunoglobulin heavy chain variable region genes obtained from a bone marrow transplant (BMT) recipient

Clin. Exp. Immunol. 107 (2), 372-380 (1997)
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/tissue_type="peripheral blood"
/note="CD19+ peripheral blood B cells obtained from a
/healthy subject; clone 104 in reference 1"
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/protein_id="AAC51094.1"
/db_xref="G1:1791201"
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/gene="V4-4b"
/note="Ig VH4 heavy chain"
/codon_start=1
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/mol_type="genomic DNA"
/db xref="taxon:9606"
/chromosome="14"
/map="1432-q33"
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2 (bases 1 to 373)
Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.
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Wakaryota, Metazoa; Chordata, Craniata, Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Macaca.

1 (bases 1 to 373)

Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Blancher,A.

and Capra,J.S.
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                                                                                     /gene="CDR1"
/note="complementarity-determining region 1; putative"
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Hybridomas Producing Human Red Blood Cell-Specific Antibodies:
Predominance of the VH4 Family but not VH4-21 (V4-34)
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9
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/gene="complementarity-determining
/note="complementarity-determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 72.9%; Score 266.8; DB 9; Best Local Similarity 84.4%; Pred. No. 2e-66; Matches 314; Conservative 0; Mismatches 52;
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  91. .108
/gene="CDR1"
91. .108
                                                                                                                                                                                           151. .201
/gene="CDR2"
                                                                                                                                                                    /gene="CDR2"
151. .201
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                                                                                                                                               151, .201
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KEYWORDS
SOURCE
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/product='immunoglobulin gamma"
/protein id="AAAAB103.1"
/db_xref='dI:293119'
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GSYIRDNSLDVWGRGVLVTVSSASTKGPSVPFLAPSSRSISSSTAALGCLVKDYFPPEP
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DKRVEIKTGCGSKFPRCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
SQEDPDVKFNWYNGAEVHHARETQYNSTYRVVSLTVTHQDMLNGKEYTCKVSNKAL
PAPLQKTISKOKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDIVVEMESSGG
PENTYKTTPPVLDSDGSYFLYSKLTVDKSRNQQGNVFSCSVMHBALHNHYTQKSLSVS
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                                                                                                                                                                                                                                                                                                                 240
                                   117
                                                                                        120
                                                                                                                                                                                                    CCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCCACCAAC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGAT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTC 360
                                                                                                                                            ACCTGCGCTGTCTCTGGTTACTCCATCAGCAGTGGTTATGGCTGGAACTGGATCCGCCAG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cynomolgus monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complementarity-determining region; constant region; heavy chain; immunoglobulin gamma; variable region.
Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.

1 (bases 1 to 1359)
Lewis, A.P., Barber, K.A., Cooper, H.J., Sims, M.J., Worden, J. and
TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source text: Macaca fascicularis cDNA to mRNA.
Location/Qualifiers
1. .1359
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94131152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1359 bp
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/db_xref="taxon:9541"
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L13307.1 GI:293118
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MACIGHVCDR
LOCUS
DEFINITION
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VERSION
KEYWORDS
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MEDLINE
PUBMED
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AUTHORS
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SOURCE

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HSUB0180
LOCUS HSUB0180 368 bp DNA linear PRI 19-FEB-1997
DEFINITION Human immunoglobulin heavy chain variable region (V4-t4b) gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="QVQLQESGPGLVKPSGTLSLTCAVSGGSISSSNWMSWVRQPPGK
GLEWIGEIYHSGSTNYNPSLKSRVTISVDKSKNQFSLKLSSVTAADTAVYYCARDMAI
FGVVIMFGYWGQGTLVTVSS"
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                                                                                                                                             Direct Submission
Submitted (11-JAN-2000) Dono M., Istituto Nazionale per la Ricerca
sul Cancro, Immunologia Clinica, L.go Rosanna benzi 10- Genova,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCCCAGGGAAGGGGCTGGAGTGGATTGGGGAAATCTATCATA---GTGGGAGCACCAAC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 TGGGCCCAAAT---AGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACC 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198 AIGGCGAITTITGGAGTGGTTAITATGTTCGGGTACTGGGGCCAGGGAACCCTGGTCACC 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="immunoglobulin mu heavy chain variable region"
/protein_id="CAB66350.1"
/db_xref="GI:6723538"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="immunoglobulin mu heavy chain variable region" 98 c 114 g 79 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGGGACCCTGTCCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="14"
/clone="CD27low-8"
/call_type="IgD-low SE B-lymphocyte"
/rearranged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.0%; Score 263.4; DB 9;
85.9%; Pred. No. 1.9e-65;
J. Immunol. 164 (11), 5596-5604 (2000)
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                                                                                                                                                                                                                                                                                                         1. .366
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                  Location/Qualifiers
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/gene="IGHV4-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="IGHV4-4"
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/gene="IGHV4-4"
                                                                                       (bases 1 to 366)
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                                                                  10820234
                                                                                                                        Dono, M.
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ORIGIN
   JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
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AJ279520 AJ279520. GI:6723537 IgM heavy chain; immunoglobulin mu heavy chain; variable region.
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Chiorazzi,N. and Ferrarini,M.
Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic
marginal zone equivalents
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PPGKGLEWIGYIVVNSGSTDYNPSLKSRVTISKDTSKNQFSLKLSSVTAADTAVYYCA
RARRGSSYVDYWGQGYLVTVSS"
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         and Capra, J.D.

Bloed: Submission
Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
University of Texas Southwestern Medical Center, 6000 Harry Hines
Blvd., Dallas, TX 75225-9140, USA
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                        <1. .>373
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/note="hybridoma"
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Best Local Similarity 85.0%;
Matches 311; Conservative
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/translation="MKHLMFPLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVS
GGSFSSYWWGWIRQPPCKGLEWIGSIYGSSGSFEYNPSLKSRATISRDTSKNQFSLKV
SSVTAADTAVYCARGDYSSNWWYFFFWGQGALVTVSS"

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1 (bases 1 to 420)
Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Roubinet, F., Blancher, A. and Capra, J.D.

Parncher, A. and Capra, J.D.

Variable region gene segment utilization in rhesus monkey hybridomas producing human red blood cell-specific antibodies: predominance of the VH4 family but not VH4-21 (V4-34)
MO1. Immunol. 34 (3), 237-253 (1997)
                                                                                                                                                                                                                                                                                      PRI 11-FEB-1998
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אמכמכת mulatta Ig rearranged heavy chain variable region, anti-RBC antibody, mRNA, partial cds.
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298 AGGGTATTGTAGTAGTACCAGCTGCAAAATTTGACTACTGGGGCCAGGGAACCCTGGTCA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 420)
Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.
and Capra, J.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
University of Taxas Southwestern Medical Center, 6000 Harry Hines
Blvd., Dallas, TX 75235-9140, USA
Location/Qualifiers
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84.2%; Pred. No. 4.7e-65;
ive 0; Mismatches 55; Indels
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Macaca mulatta
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                                                              356 CCGTCTCCTCA 366
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358 CCGTCTCCTCA 368
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Matches 308;
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Direct Submission
Submitted (29-NOV-1996) Immunology; Virginia Mason Research Center, 1000 Seneca Street, Seattle, WA 98101, USA
Location/Qualifiers
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GLEWIGEIYHSGSTNYNPSLKSRVTISVDKSKNQFSLKLSSVTAADTAVYYCARDRVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCCTGAACCTGAACTCTGTGACCGCGGGGCGCGCGTGTATTACTGTGCCAGAGAT 300
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(Dases 1 to 368)

Glas,A.M., Nottenburg,C. and Milner,B.C.
Analysis of rearranged immunoglobulin heavy chain variable region genes obtained from a bone marrow transplant (BWT) recipient
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/tismsue_type="peripheral blood"
/noce="CD19+ peripheral blood B cells obtained from a
healthy subject; clone 105 in reference 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="immunoglobulin heavy chain variable region"
protein_id="AAC51095.1"
db_xref="GI:1791203"
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Pred. No. 2.4e-65;
0; Mismatches 45;
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/note="Ig VH4 heavy chain"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="14"
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85.7%;
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U80180.1 GI:1791202
                                                                                                                               Homo sapiens (human)
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Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A., Chiorazzi, N. and Ferrarini, M. Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic marginal zone equivalents
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/codon_start=1
/product=1,immunoglobulin mu heavy chain variable region"
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/db_xref="G1:4995523"
/db_xref="G1:4995523"
/db_xref="G1:4995523"
/db_xref="GNQDESCOFGLVKFSGTLSLTCAVSGGSISSSNWWSWVRQPPGKGLEWIGSIXYSGSTYNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARHEYS
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variable
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Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca
sul Cancro, Immunologia Clinica, L.go Rosanna benzi 10- Genova,
                                                                                                                       241 TCCCTGAACCTGAACTCTGTGACGCGCGCGGGCCGTGTATTACTGTGCCAGAGAT 300
                                                                                                                                          295 TCCCTGAAGCTGAGCTCTGTGACCGCCGCGGAGCAGGCCGTGTATTACTGTGCGGAGGTAT 354
                                                                                                                                                                                                                            301 TGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTC 360
175 CCCCCAGGGAAGGGACTGGAGTTGGACGTTTCTATGGTACTAGTGGAGCACCTAC 234
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                          181 TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACAGTCCAAGAACCAGTTC
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IgM; IgM heavy chain; immunoglobulin mu heavy chain; variable
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/cell_type="B-lymphocyte"
/tissue_type="tonsil"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="14"
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/gene="IGHV4-4"
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/gene="IGHV4-4"
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/gene="IGHV4-4"
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Homo sapiens
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Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.

1 (bases 1 to 411)
Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Roubinet,F.,
Blancher,A. and Capra,J.D.
Marncher,A. and Capra,J.D.
Variable region gene segment utilization in rhesus monkey
hybridomas producing human red blood cell-specific antibodies:
predominance of the VH4 family but not VH4-21 (V4-34)
MO1. Immunol. 34 (3), 237-253 (1997)
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GGSISSNYWSWIRQPPCKGLEWIGRFYGTSGSTYYNPSLTSRVTISTDTSKNQFSLKL
SSSYTAADTAVYZCARYTVSKAFDYWGGGVLVTVSS"
124 C 115 g 91 t
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Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC
antibody, mRNA, partial cds.
                                                                                 301 TGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACGGTC 360
355 GACTACAGTAGCAACTGGTGGTACTTCGAGTTCTGGGGCCAGGGCGCCCTGGTCACGTC 414
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      TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGAT 300
                           295 TCCCTGAAGGTGAGCTCTGTGACCCCCCGGACACGGCCGTGTATTACTGTGCGAGAGGA 354
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Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.
and Capra, J.D.
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Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
University of Taxas Southwestern Medical Center, 6000 Harry Hines
Blvd., Dallas, TX 7525-9140, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CAGCTGCAGCTGCAGGAGTCGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC
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/db_xref="GI:1575074"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .411
/organism="Macaca mulatta"
/mol_type="mRNA"
/db_xref="taxon:9544"
/note="hybridoma 1B4"
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Macaca mulatta
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Matches 316; Conserv
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GTCTCCTCA 423
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H.Sapiens mRNA for XLA IG heavy chain VDJ region (LE 4-8).
X65910.158678
Giversity region; Ig heavy chain; immunoglobulin; joining region; variable region.
Homo sapiens
Homo sapiens
                                                                                                                ACCTGCGCTGTCTCTGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
                                                                                                                                  ACCTGCGCTGTCTCTGGTGGCTCCATCAGCAGTAGTAATTGGTGGAGTTGGGTCCGCCAG 120
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                                                                                                                                                                                          TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC 240
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                                                          1 CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC
                               Gaps
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Submitted (08-APR-1992) C. Schiff, Centre D'Immunologie de Marsaille, Case 906, 13288 Marsaille, Cedes 9, FRANCE 2 (bases 1 to 423)
Milli,M., Le Daist,F., de Saint-Basile,G., Fischer,A., Fougereau,M. and Schiff,C.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 423)
                              3;
   Length 363;
                            Indels
 Score 260.4; DB 9;
Pred. No. 1.4e-64;
0; Mismatches 56;
DB 9;
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/tissue_type="bone_marrow"
/clone_lib="LE library"
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organism="Homo sapiens'
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/note="variable region"
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/db_xref="taxon:9606"
/chromosome="14"
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Query Match
Best Local Similarity 83.9%;
Matches 307; Conservative
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HSIGHXX28
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MMU57568 414 bp mRNA linear PRI 11-FEB-1998
Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC
antibody, mRNA, partial cds.
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I bases i to 411 A.B., Abraham, S.R., Cunningham, S., Roubinet, F., Bancher, A. and Capra, J.D.

Rancher, A. and Capra, J.D.

Variable region gene segment utilization in rhesus monkey hybridomas producing human red blood cell-specific antibodies: predominance of the VH4 family but not VH4-21 (V4-34)

MOL. Immunol. 34 (3), 237-253 (1997)
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Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.
and Capra, J.D.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                   CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGACACCCTGTCCCTC
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/mol_type="mRNA"
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/note="diversity region"
378. .423
/note="joining region"
a 120 c 123 g 9
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/db_xref="taxon:9544"
1 .>414
1 .>414
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1 /oodom start=1
/codom start=1
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/protain_id="AACUGG45.1"
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SYSTSSNYWSWTRQPPGKGLEWTGYIYGSSGSAYYNPSLKSRVTISIDTSKNQPSLKL
SSVTAADTAVYYCRDPYGPTPYGPYGVTUTVSS"
3 128 C 110 g 93 t
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355 -----CCCTACGGTCCCACATACTTTGACTACTGGGGGCCAGGGAGTCCTGGTCACGGTC 408
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Result

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IMAGE:3053955 5', mRNA sequence.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Standt, M.D., Ph.D.
CDNA Library Arrayed by: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
CON Eco RI Strausbron: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution of MGC clone distribution of MGC clone distribution of MGC clone distribution information can be found through the I.M.AG.B. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
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5616.780 Million cell updates/sec
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                                                                                                                                                                                     December 29, 2003, 16:08:50 ; Search time 1583.73 Seconds
                                                                                                                                                                                                                                                                                                                                                    ....TCCTGGTCACCGTCTCCTCA 366
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                         GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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366
1_CAGCTGCAGCTGCAGAGTC.....
                                                                                                                                  OM nucleic - nucleic search, using sw model
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BU429270
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Gapop 10.0 , Gapext 1.0
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em_gss_vrl:*
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Maximum DB seq length: 2000000000
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680
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Perfect score:
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/moi type="mrRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="rkMcs:5761604"
/lab_host="mrMcs:5761604"
/lab_host="mrMcs:5761604"
/lab_host="mrMcs:5761604"
/lab_host="mrMcs:5761604"
/lone="dorgan: pooled lung and spleen; Vector: pCMV-SPORT6; Note="dorgan: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-inergh clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MC Library.

20 a 335 c 283 g 197 t 1 others
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 524)

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DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov row: h column: 21 Plate: LLAM12810 row: h column: 21 High quality sequence stop: 626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.1%; Score 249.2; DB 13; Length 1036; 83.9%; Pred. No. 4.4e-55; tive 0; Mismatches 53; Indels 6;

    1036
    organism="Homo sapiens"

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Homo sapiens
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_6839001 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5761604
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1036)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74.2%; Score 271.6; DB ilarity 85.8%; Pred. No. 4e-61; Conservative 0; Mismatches 4
                                                                           organism="Homo sapiens"
            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ072430.1 GI:19901476
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 ACCIGCACIGCTCTGGTGGCTCCATCAGCAGTAGTTACTTCTGGGGCTGGATCCGC 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        276 TTCTCCCTGAACCTGAGCTCTGTGACCGCGCGGACACGGCCGTATATTACTGTGCGAGA 335
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                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NIH_MGC_50"
/note="Wetcor: pT773-pac; Site_1: Not1; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(3.5-4.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "
                           Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbb=r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13; Length 524;
                                                                                                                                                                                                                                                                                              Score 247.4; DB 1.
Pred. No. 9.9e-55;
0; Mismatches 46
                                                                                                                                                                                                                                                                                organism="Homo sapiens"
                                                                                                                                                                                                                                               Location/Qualifiers
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Best Local Similarity 84.5%;
Matches 317; Conservative (
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EST 01-JUN-2003

CB551642 680 bp mRNA linear E. MMSP0006\_D02 MMSP Macaca mulatta cDNA, mRNA sequence. CB551642\_CB551642.1 GI:31300837

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BX283435 NIH MGC 48 Homo sapiens CDNA clone IMAGp958G051281 ; IMAGE:4565020, mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 502)
Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
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                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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                                                                                                                           1 (bāses 1 to 680)
Katze, M.G., Bumgarner, R., Korth, M., Feldman, R., Amjadi, M.
                                                                                                                                                                                                                                                                                                University of Washington
Box 158070, Seattle, WA 98195-8070, USA
Tel: 206 712 6156
Fax: 206 712 6055
Email: ted@locke.hs.washington.edu
Similar to GenBank entry AF062240 AF662240 Homo sapiens
23u-44 immunoglobulin heavy chain variable region (IGH)
partial cds. 2000 row: D column: 02.
Location/Qualifiers
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                                                                                                                                                                                                 Expressed sequence tags from Rhesus macaque spleen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Macaca mulatta"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="monocytes"
/dev_stage="adult"
/clone_lib="MMSP"
/note="Organ: spleen"
a 187 c 177 g 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9544"
mulatta (rhesus monkey)
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     Macaca mulatta
Macaca mulatta
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Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="primarry B-cells from tonsils (cell line)"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: Ecors; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GGACGAGG(6). Size-selected >50bp for average insert size 18kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                             RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response7libNo-972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 111
Fax: +49 30 32639 111
                                                                 GmbH
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                                               Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung
IN Nevenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGD958G051281.
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                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.2%; Score 246; DB 13;
ilarity 83.3%; Pred. No. 2.3e-54;
Conservative 0; Mismatches 55;
   Radelof, U., Schneider, D. and Korn, B.
                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
             Human UnigeneSet - RZPD3
Unpublished
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Matches
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ORIGIN
                TITLE
JOURNAL
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/clone lib="MIH MGC Bost Xite l: Xho!;
Site 2: Ecosl: CDNA made by oligo-dT priming.
Site 2: Ecosl: CDNA made by oligo-dT priming.
Borectionally cloned into Ecost XiXno site using the for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald Mr. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MCC Library."
862 bp mRNA linear EST 12-MAR-2001
mRNA sequence.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can bettp://image.llnl.gov
pttp://image.llnl.gov
g column: 05
High quality sequence stop: 827.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele:
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 862)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                         BG397580.1 GI:13291028
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// clone lib="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: BCORI, cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis Kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                               BQ710000 921 bp mRNA linear EST 16-JUL-2002 AGENCOURT 8495271 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6302029 5', mRNA sequence.
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  35 TTCTCCCTGAGGCTGAGCTCTGTGACCGCCGCGACACGCCCGTGTATTACTGTGCGAGT 414
                                                                                  415 GGTTGTAGTGGTGGTGCTGCCTCGCCTTTGACTACTGGGGCCAGGGAACCCTGGTC 474
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bakaryota; Metazoa; Craniates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 921)
NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGCTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CAGCTGCAGCTGCAGGAGTCGGGCCCCAGGAGTGAAGCCTTCGGAGACCCTGTCCCTC
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Pred. No. 8.6e-54;
0; Mismatches 58; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMX518 row: n column: 14
High quality sequence start: 10
High quality sequence stop: 604.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
Contact: Robert Strausberg, Ph.D.
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Best Local Similarity 82.7%;
Matches 305; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
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                                                                                                                                 355 ACCGTCTCCTCA 366
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BP 191 91006 EVRY cadex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
eggl-bin/cluster.cg1?seq=CS0A1086CED7Opl&cluster=7198.r. Contact:
Forg Liang Email: fliangdelifetech.com URL:
http://fulllength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOA1086CE07QPl.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Pull-length cDNA libraries and normalization
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Genoscope - Centre National de Sequencage
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Enkaryota, Metazoa; Chordata, Catarrhini; Hominidae; Homo.

1 (Dases 1 to 925)
1 (Dases) 1 to 925)
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1 (Machini Metazoa) Hominidae; Homo.

2 NH-MGC http://mgc.nci.nih.gov/.

3 NH-MGC http://mgc.nci.nih.gov/.

3 Unpublished

4 Contact: Robert Strausberg, Ph.D.

5 Email: cgapbs-remail.nih.gov

7 Tissue Procurement: Dr. Mark Watson

6 Contact: Robert Strausberg, Ph.D.

7 Saul Strausberg, Preparation: Rubin Laboratory

6 Contact: Robert Strausberg, Ph.D.

7 Saul Strausberg, Preparation: Mark Matson

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/tissue_type="primary B-cells from tonsils (cell line)"
/issue_type="primary B-cells from tonsils (cell line)"
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/clone line="MIH MGG 48"
/note="Organ: B-cells, Vector: porB7; Site_1: XhoI;
Site_2: EcoR1; cDNA made by Oilgo-dT priming.
Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected -550bp
for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: Library."
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

L Umpublished

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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Http://image.llnl.gov

Plate: LLCMI623 row: a column: 21

High quality sequence stop: 637.
   237
                                                                                                                                                                                             298 GATTGGGCCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACC 357
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 867)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG685428 867 bp mRNA linear EST 01-MAY-20
G00537281F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4764956 5',
AACTACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAG
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/organism="Homo sapiens"
/clone="DKFZp686M10219"
/clone="DKFZp686M10219"
DH10B-sites SilA + SfilB"
/dev_stage="adult"
/tissue_type="cDNA-collection"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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con Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.lnl.gov
http://image.lnl.gov
Blate: LLCMS18 row: b column: 18
High quality sequence start: 12
High quality sequence stop: 587.
I.ocation/Qualifiers
I. 939
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                        Length 532;
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                                                                                                                                                                           Sequence 532 BP; 108 A; 163 C; 142 G; 114 T; 5 other;
                                                                                                                                                                                                                    Score 241.6; DB 2;
Pred. No. 3.4e-53;
0; Mismatches 60;
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
/mol type="mRNA"
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Ottenwaelder B., Obermaier B., Deutschenbaur S., Mewes H.W., Weil
Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the 5' sequence of the clone insert Clone from S. Wiemann, Wolecular Genome Analysis, German Cancer Research Center (DKTS); Email s.wiemann@dkfz-heidelberg.de; sequenced by MediGenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project.

81 sequence also available.
This clone (DKFZp686M10219) is available at the RZPD in Berlin.
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                     59; Indels
82.4%; Pred. No. 2.3e-53;
ive 0; Mismatches 59
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/mol_type="mRNN"
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UI-HF-BLO-aco-h-03-0-UI.r1 NIH MGC_37 Homo sapiens cDNA clone
IMAGE:3059933 5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seg primer: M13 Forward.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.4%; Score 239.4; DB 5
llarity 90.2%; Pred. No. 1.3e-52;
Conservative 0; Mismatches 26
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                                                                                                                                                                                                                                                             /organism≃"Homo sapiens"
                                                                                                                                                                           Location/Qualifiers
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nes 268; Conserv
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AUTHORS
TITLE
JOURNAL
COMMENT
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                                                                                                                            /clone="IMAGE:331745"
/lab_host="IMAGE:331745"
/lab_host="DH10B (phage-resistant)"
/clone=lib="NH1 MGC_113"
/clone=lib="NH1 MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into ECORI/AhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superseript II RT (Life Technologies). Note: this is a
NIH MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117
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11 (bases 1 to 515)
11 hGr.htp://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 6e-53;
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Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab
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                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
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Homo sapiens
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/cell_type="lymph"
/cell_type="lymph"
/cell_time="MGG85"
/lab_host="DHJDB (LTI)"
/clone_lib="NIH MGC 37"
/note="Vector: pT773-Pac; Site_l: NotI; Site_2: Eco RI;
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/note="Vector: pT773-Pac; Site_l: NotI; Site_2: Eco RI;
/constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. 146 g 98 t
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BX337642 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI044YB21 5-PRIME, mRNA sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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84.0%; Pred. No. 2e-52;
ive 0; Mismatches 44; Indels 15
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
www-bio.llnl.gov/bbrp/image/image.html
                                                        1. .509
/organism="Homo sapiens"
                                                                                              (mol_type="mRNA"
| db_xref="taxon:9606"
| clone="IMAGE:3059933"
                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cissue type="PLACENTA COT 25-NORMALIZED"
/close lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCNWSPORT 6 vector. Library was normalized.
                                                                                                                  http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODIO44CAllQPl&cluster=7198.r. Contact
cgi-bin/cluster.cgi?seq=CSODIO44CAllQPl&cluster=7198.r. Contact
peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIO44CAllQPl.
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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198.r
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
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Pred. No. 2.7e-52;
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                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI044YB21"
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ilarity 81.1%;
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Matches 309; Conserv
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Anti-CD4 antibody Monkey anti-CD4 he DNA encoding cynom Human diagnostic a

Heavy chain DNA fr Human lung cancer

ebvHigM MSI19D10 h

Nuclectide sequenc Anti-CD40 monoclon EST clone 099. Ho Germine anti-IGF-Monkey anti-human Monkey anti-CD4 he

Scoring table:

Searched:

Database

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Anti-CD4 antibody
Multiple sclerosis
Human bladder tumo
Human immunoglobul
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Anti-human CD23 6G5 moclonal antibody heavy chain variable region DNA.
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/note= "encodes CDR 1 region"
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AAZ39335
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ABS73187
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(c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                            The present sequence represents a DNA sequence encoding the heavy chain variable region of primate monoclonal antibody anti-buman CD23 dGS. The invention provides primate monoclonal antibodies which specifically bind human CD23, the low affinity receptor for IGE (FceRii/CD23), and comprise either of a human gamma-1 or human gamma-3 constant region that binds to human Fc gamma receptors and inhibits IGE expression. The monoclonal antibodies of the invention are claimed to be useful for inhibiting induced IGE production for treating or preventing for inhibiting and autoimmune conditions e.g. allergic rhinitis conjunctivitis, autoimmune hasmolytic anaemia, etc. (Updated on 25-MAR-2003 to correct PR field.)
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Best Local Similarity
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 misc_feature
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                                                                                                                                                                                                                                                                                                                                                                  Primatised anti-human B7.1 antigen antibody 16C10 heavy chain DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monoclonal antibody; cynomolgus monkey; macaque; 16C10; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenia purpura; systemic lupus erythematosus; rheumatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease; hetero-hybridoma; transfectoma; ss.
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AAT62513 standard; DNA; 1431
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P-PSDB; AAW01822.
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Best Local Similarity
Matches 313; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence encodes a primatized form of the antibody 16C10 heavy chain from macaque. This sequence is used in a method which studies new monoclonal antibodies (Mab's) that bind selectively to 87.1 (CD80) or to 87.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such Mab's are specific immunosuppressants for treatment of diseases involving 1 cell/B cell interactions, particularly autoimmune disease, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple sclerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours Optionally the MAb can be conjugated to a during or toxin. MAb's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop
                                                357
                        TCCCTGAACCTGAACTCTGTGACCGCCGCGGGCCCCTGTGTTACTGTGCCAGAGAT 300
                                                                       TGGGCCCAAATAGCTGGAACAA------CGCTAGGCTTCTGGGGCCAGGGA 345
                                                                                              cercrititicaerierregaareerrracaacaacreerresarereisesesecessa 417
                                                                                                                                                                                                                                                                                                         Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
 238 TACAACCCCTCCAAGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B cells, e.g. graft rejection or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= 16C10 heavy chain
                                                                                                                                                                                                                                                                                 Macaque primatized 16C10 heavy chain DNA.
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                       GTCCTGGTCACCGTCTCCTCA 366
                                                                                                                                              GreeredreAccererera 438
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P-PSDB; AAW63765.
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anti-idiotype reagents. MAb's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 (IL-2), T cell proliferation and antigen-specific immunoglobulin G (IgG) responses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA sequence of a primatised form of the heavy chain of 16C10 antibody.
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 250.1.,
Pred. No. 6.1e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 82.2
Matches 313; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric - Homo sapiens.
Chimeric - Macaca sp.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                             idiopathic thrombocytopenia purpura, systemic lupus, erythematosus, type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bile disease, allergy, multiple sclerosis or graft-ve-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or rejection of transplanted organ or tissue for treating proliferative and hyperproliferative diseases, for treating reversible obstructive airways disease, intestinal inflammations and allergies e.g. Crohn, thinlies and ulcerative colitis, food-related allergies e.g. migraine, thinlits and eczema, and other types of allergies. The present nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accrececrerereresisericareacesiserraneseriseseriseareceas
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                                                                                                                                                                 Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acid sequence encodes the heavy chain of 16\text{Cl}\tilde{0}, a primarised antibody used in the invention to induce apoptosis and inhibit production of
                                                                                                                                                                                                                                                                                                The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen (CD86) for inducing the apoptosis of B7+ cells. The invention is useful for treating diseases such as B cell cancer, lymphoma, a cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma. B cell leukaemia, and autoimmune diseases such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 24; Length 1431;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 256.2; DB 2.
Pred. No. 6.1e-61;
0; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCCTGGTCACCGTCTCCTCA 438
                                                                                                                                                                                                                                                                Example 8; Fig 5b; 89pp; English.
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                                                                         Brams
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.2%;
22-MAY-2000; 2000US-0576424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 313; Conservative
                                    PHARM CORP
                                                                         Hanna N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interleukin-2 (IL-2)
                                                                                                              WPI; 2002-089895/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                  P-PSDB; AAU11646.
                                    (IDEC-) IDEC
                                                                         Anderson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298
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TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGAT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention provides an antibody (Ab) comprising donor CDRs (complementarity determining regions) derived from a non-human antigenspecific donor antibody, and an acceptor framework from a non-human primate. The Abs are prepared by grafting CDRs from a non-human human specific donor antibody onto homologous Old World ape or monkey acceptor frameworks. The Abs have reduced immunogenicity and are better tolerated in humans (because of the close similarity between the human and primate process), but retain the full antigen-binding affinity of the donor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibodies containing donor complementarity determining regions and non-human primate acceptor frameworks, having reduced immunogenicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21; Length 423;
                                                                                                                             Complementarity determining region; antibody; primate; immunog old World ape; Old World monkey; antigen-binding affinity; se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                              Nucleotide sequence of Cynomologous VH cDNA clone 2-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 423 BP; 76 A; 125 C; 122 G; 100 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.6%; Score 247.4; DB 21; ilarity 83.2%; Pred. No. 1.2e-58; Conservative 0; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Page 79; 123pp; English
                                                                                                                                                                                                                                                                                                                                           (SMIK ) SMITHKLINE BEECHAM CORP.
BP.
                                                                                                                                                                                                                                                                              99WO-US09131.
 DNA; 423
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-023265/02.
P-PSDB; AAY56663, AAY56728.
                                                                  (first entry)
 AAZ39331 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 307; Conserv
                                                                                                                                                                                 Macaca cynomolgus
                                                                                                                                                                                                                W09955369-A1
                                                                                                                                                                                                                                                                              28-APR-1999;
                                                                                                                                                                                                                                                                                                              28-APR-1998;
                                                                  15-FEB-2000
                                                                                                                                                                                                                                              04-NOV-1999
                                 AAZ39331;
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TCCCCAGGGAAGGGACTGGAGTGGATGGGTACATCTATGGCAGTGGTGGGGGCACCAAT 237
                                                                                                                                                  241 TCCCTGAACCTGAACTCTGTGACGCCGCGGGCGGCCGTGTATTACTGTGCCAGAGAT 300
                                                                                                                                                                                                                                     301 TGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTC 360
                                                                                                                                                                                                                                                             ---ATATTGAAATATCTTCACTGGTATATTATACTGGGGCCAGGGAGTCCTGGTCACCGTC 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA sequences (AAT62868-70) respectively code for the heavy chain regions of human gamma-4 (AAW14925), gamma-4E carrying the L236E mutation (AAW14926) and gamma-4PE (AAW14927) carrying L236E and S229P mutations. They can be used to provide novel monoclonal and chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in which the human 19G4 Fc binding domain framework is combined with the antigen binding domains (see also AAW14922-23) of macaque anti-human CD4 monoclonal antibody E9.1. These antibodies show high affinity to human CD4, have little or no immunogenicity in humans and show reduced or absence of effector function. The
                                                                                         TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD4; monoclonal antibody; chimaeric antibody; recombinant antibody; cynomolgus monkey; autoimmune disease; rheumatoid arthritis; leukaemia; lymphoma; graft-versus-host disease; asthma; transplant rejection; HIV; therapy; CB9 gamma-4E; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gamma-4E and -4PE mutations confer activity enhanced stability and eliminate depleting activity. The antibodies can be used to treat autoimmune diseases such as rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric antibody comprising monkey variable domains and human constant domains - affects CD4-mediated immune functions, espuseful for treatment of autoimmune disease, e.g. rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 86-88; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT62869 standard; DNA; 1404 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human gamma-4E heavy chain DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reff ME;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-OCT-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IDEC-) IDEC PHARM CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-201913/18.
P-PSDB; AAW14926.
                                                                                                                                                                                                                                                                                                                                                                    TCCTCA 420
                                                                                                                                                                                                                                                                                                                           TCCTCA 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 ACCTGCAGTGTCTCTGGTGGCTCCATCAGCGGTGACTATTATTGGTTCTGGATCCGCCAG 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA sequences (AAT62868-70) respectively code for the heavy chain regions of human gamma-4 (AAM14925), gamma-4 Rearrying the L236E mutation (AAM14926) and gamma-4FE CARNYING LD 1336E mutation (AAM14926) and gamma-4FE (AAM14927) carrying L236E and S229P mutations. They can be used to provide novel monoclonal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC
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                                                                                                                                                                                                                                                                                                                                                  CD4; monoclonal antibody; chimaeric antibody; recombinant antibody; cyromolgue monkey; autoimmune disease; rheumatoid arthritis; leukaemia; lymphoma; graft-versus-host disease; asthma; transplant rejection; HIV; therapy; CE9 gamma 4; ss.
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Pred. No. 4e-58;
0; Mismatches 65; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1404 BP; 312 A; 448 C; 377 G; 267 T; 0 other;
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                               GICTCCTCA 366
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P-PSDB; AAW14925.
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                                     3;
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                  DB 18; Length 1404;
                                     Indels
Sequence 1404 BP; 313 A; 446 C; 379 G; 266 T; 0 other;
                                     65;
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                                     0; Mismatches
               tch 67.2%; Score 246; sal Similarity 81.4%; Pred. No. 46. 298; Conservative 0; Mismatche
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P-PSDB; AAW14927.
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/*t.gg= a
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/*tag= b
/*tote= "light chain variable region coding sequence"
331..747
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DNA sequences (AAT62868-70) respectively code for the heavy chain regions of human gamma-4 (AAM14925), gamma-4E carrying the L236E mutation (AAM14926) and gamma-4PE (AAM19297) carrying L236E and S22 mutations. They can be used to provide novel monoclonal and chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in which the human IgG4 Fc binding domain framework is combined with the antigen binding domains (see also AAM14922-23) of macaque anti-human CD4 monoclonal antibody E9.1. These antibodies show high affinity to human CD4, have little or no immunogenicity in humans and show reduced or absence of effector function. The gamma-4E and -4PE mutations confer activity enhanced stability and eliminate depleting activity. The antibodies can be used to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide sequence of antibody directed against K293 superantigen.
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ص
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1404 BP; 313 A; 447 C; 379 G; 265 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                        eliminate depleting activity. The antibodies can autoimmune diseases such as rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 246; DB 18
Pred. No. 4e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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coding sequence.

(updated)
(first entry)

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PCR; amplify; clone; heavy; light; chain; variable; region; lambda; immortalised B-cell; vector; TCAB 6; human; 1gG1; constant; antigen; recombinant; antibody; chimpanzee; 1g; Ag; old world monkey; eczema; immunoglobulin; therapeutic; rheumatoid arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant antibodies including Old World monkey portion ar
human portion - used for treatment of auto-immune diseases,
infectious diseases, AIDS, tumours, diabetes, proliferative
diseases, intestinal inflammations and allergies, etc.
                                                                                                                                                                                                                                                                                                                                        (IDEC-) IDEC PHARM CORP
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P-PSDB; AAR31948.
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                                                                                                                                                                                                       WO9302108-A1
                                                                                                                                                                                                                                                                                                           23-MAR-1992;
                                                                      Anti-CD4 VH
                           25-MAR-2003
08-JUN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention provides a binding structure, such as an antibody, binding to tumor cells, especially epithelial tumor cells such as colorectal, pancreatic, breast or lung carcinoma cells. The binding structures, target structures to the binding structures or the substances, i.e. antisense oligonucleotides and ribozymes, are useful in the therapy and in vitro histopathological diagnosis and prognosis of human malignant disease. The present sequence represents the nucleotide sequence of antibody directed against K293 superantigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGC 121
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    - GATAGAGGCTGGCACGAATACTTCGACTTCTGGGGCCAGGGAGTCCTGGTCACCGTTT 742

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 /*tag= c
/note= "heavy chain variable region coding sequence'
                                                                                                                                                                                           Tordsson MJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.9%; Score 245; DB 22; Length 747; 83.3%; Pred. No. 6.4e-58;
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                                                                                                                                                                                           Ohlsson LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                           Nilson BHK,
                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 70-71; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 83.3%;
Matches 304; Conservative
                                                                                                     23-FEB-2001; 2001WO-SE00395.
                                                                                                                                 2000SE-0000597.
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                                                                                                                                                              (ACTI-) ACTIVE BIOTECH AB
                                                                                                                                                                                           Brodin TN, Karlstroem
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                                                                        30-AUG-2001
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Raab RW

Newman RA,

92WO-US06194 91US-0735064 92US-0856281

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                                       The sequences given in AAQ35903-04 encode the Simian anti CD4 VH and V-lambda sequences respectively. These sequences were derived using the primer sequences given in AAQ35901-02. The amplification products were sequentially cloned into the vector TCAE 6, which contains human 1961 and human lambda constant regions. The amplified sequences could human, chimpanzee or old world monkey immunoglobulin (1g) constant region and an antisped May binding portion of an old world monkey if a varible region, where the old world monkeys may be the same or different. The recombinant antibody may be used as a therapeutic agent for the treatment of rheumatoid arthritis, eczema and immunological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.8%; Score 244.4; DB 14; Length ilarity 81.1%; Pred. No. 8.2e-58; Conservative 0; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                               (Updated on 25-MAR-2003 to correct PN field.)
Disclosure; Page 53-54; 92pp; English.
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Best Local Similarity
Matches 297; Conserv
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RESULT 10 AAQ35903 ID AAQ3 XX

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ACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
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/trag= a
/transl_except= (pos:415..417, aa:Ser)
/product= "Variable heavy chain antigen binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-CD4 antibody variable heavy (VH) region encoding DNA.
Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;
                                                    Score 244.4; DB 1:
Pred. No. 8.2e-58;
0; Mismatches 66
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Chimeric - Homo sapiens.
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91US-0735064.
92US-0856281.
92US-0912292.
95US-0379072.
                                                       Query Match 66.8%;
Best Local Similarity 81.1%;
Matches 297; Conservative (
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10-JUL-1992;
25-JAN-1995;
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     TCCCTGAACCTGAACTCTGTGACCGCGCGCGGACACGCCCGTGTATTACTGTGCCAGAGAT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-CD4 cynomolgus monkey immunoglobulin heavy chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-CD4 antibody; cynomolgus monkey; immunoglobulin; Ig; chimpanzee; chimeric antibody; human therapy; Old World monkey; antigen binding region; tumour; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= Anti-CD4_VH_region
/note= "No stop codon_given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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91US-0735064.
92US-0856281.
95US-0379072.
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(first entry)
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                                                                                                                                                                                                                                      TCCTCA 366
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25-JAN-1995;
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16-JAN-1998
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Hanna N, Newman RA, Raab RW;

(IDEC-) IDEC PHARM CORP.

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mat_peptide
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                                                                                                                                                                                                                                                                                    ACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
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                                                                                                                                                                                                                                                                                                                                CCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTCTGGTAGTGGTGGGGGCCACCAAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer; PCR; amplification; leader sequence; human; monkey; baboon; macaque; immunoglobulin; heavy chain variable region; chimpanzee; hybrid; lymphoma; AIDS; autoimmune disease; inflammatory disease; transplant;
                                                                                                This DNA encodes the heavy chain variable region (VH) of the cynomolgus monkey anti-CD4 antibody. The antibody comprises antigen-binding sequences from an Old World monkey antibody and human constant domain sequences. The antibody specifically binds to CD4 and can be used in the treatment of rheumatoid or psoriatic arthritis.
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/note= "no stop codon given at the 3' end of sequence"
                                                                                                                                                                                                                                                                                                                                                                                              TACAATCCCTCCCTCAACAATCGAGTCTCCATTTCAATAGACACGTCCAAGAACCTCTTC
                                                                                                                                                                                                                                       1 CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC
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                                                                                                                                                                                           DB 19; Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monkey anti-CD4 heavy chain variable region coding sequence
                                           Treatment of rheumatoid and psoriatic arthritis - comprises administration of chimeric human-monkey anti-CD4 antibody
                                                                                                                                                                                                                  66; Indels
                                                                                                                                                                      Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;
                                                                                                                                                                                           Score 244.4; DB 1
Pred. No. 8.2e-58;
                                                                                                                                                                                          Query Match 66.8%; Score 244.4; Best Local Similarity 81.1%; Pred. No. 8.2e Matches 297; Conservative 0; Mismatches
                                                                            Claim 2; Columns 35-36; 47pp; English
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                     P-PSDB; AAW57446
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81.1%; Pred. No. 8.2e-58;
""" """ """ Indels
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92US-0856281
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es 297; Conserv
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Pred. No. 8.2e-58; 0; Mismatches Score 244.4;

66.8%; 81.18;

DB 25; Length 423;

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Query Match
Best Local Similarity 81.13
Matches 297; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant chimeric antibodies comprising human, chimpanzee and Old World monkey portions, useful for treating e.g. cancer, eczema, leukemia, lymphoma, Hashimoto's thyroiditis, multiple sclerosis or ma
                                                                                                                                                                                                                                                 Old world monkey; monkey; tumour; cancer; ds; immunoglobulin variable region; immunoglobulin variable region; autoimmunos espone; rheumatoid arthritis; eczema; lymphoma; immunomodulatory disease; leukaemia; Hashimoto's thyroiditis; autoimmune carditis; Addison's disease; type I-diabetes mellitus; multiple sclerosis; male infertility; autoimmune hemolytic anaemia; inflammatory bowel disease; Sjogren's syndrome; psoriasis;
                                                                                                                                                                                                                  cynomolgus monkey immunoglobulin heavy chain.
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                                                                                                                  ABX76616 standard; DNA; 423 BP
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95US-0476237.
98US-0082472.
91US-0735064.
92US-0856281.
95US-0397072.
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P-PSDB; ABU56789.
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07-JUN-1995;
21-MAY-1998;
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17-APR-1995;
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CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC
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99US-0156294.
99US-0156654.
99US-0156624.
99US-0167410.
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99US-0167520.
99US-0167943.
99US-0167943.
99US-0168197.
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30-NOV-1999;
30-NOV-1999;
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Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;

recombinant antibody

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The present sequence for human diagnostic and therapeutic (dithp) cDNA sequence #37 is 1 of 71 (AAS03012-AAS03082) novel sequences described in the invention. The present sequence (Incyte ID No: 4442487dec) cancedes an antigen recognition molecule. The dithp polymucleotides may be used to diagnose a condition disease or disorder associated with human molecules. They can be used to identify the presence of similar nucleic acids. Dithp polymucleotides may used to generate hybridisation probes for use in chromosomal mapping. Polypeptides (DITHP) encoded by dithp are used to screen for molecules which bind to them and modulate their activity. Dithp polymucleotides can be used for gene therapy of disorders such as severe combined immunodeficiency syndrome (SCID), cystic fibrosis, thalassemia, haemophila resulting from Factor VIII cystic fibrosis, thalassemia, haemophila resulting from Factor VIII hypercholesterolaemia (FH), cell proliferative disorders e.g. cancers,
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infectious disorders and developmental disorders. The antibodies can be
                                                                                                                                                                                                                                                                                                                                                     Yap PE, Stockdreher TK;
                                                                                                                                                                                                                                             Banville SC;
Shah P, Chalup MS;
Panzer SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel diagnostic and therapeutic polynucleotides, used in disease diagnosis and for gene therapy of conditions such as cancer and thalassemia
                                                                                                                                                                                                                                             Russo FD, Spiro PA,
Cohen HJ, Rosen BH,
Yu JY, Greenawalt LB,
J, Chen W, Liu TF, Ya
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                                 99US-0168432.
99US-0168468.
99US-0168599.
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99US-0168429
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Bratcher SR, Duruman JL, Jones AL, Yu
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                                 30-NOV-1999;
01-DEC-1999;
01-DEC-1999;
30-NOV-1999;
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DB 22; Length 619; Score 244.2; DB 22; Length Pred. No. 1e-57; 0; Mismatches 58; Indels Sequence 619 BP; 121 A; 192 C; 176 G; 130 T; 0 other; Query Match
Best Local Similarity 82.7%;
Matches 305; Conservative (

Gaps

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152
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1 CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC
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Search completed: December 29, 2003, 16:25:37 Job time : 161.688 secs

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Sequence 110, App Sequence 114467, Sequence 114467

Sequence

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Sequence 3, Apl Sequence 3, Apl Sequence 2, Apl Sequence 110,

1183, Ap 59, Appl

Sequence 59, Sequence 11, Sequence 9, Sequence 111

Sequence:

Run on:

Searched:

Database

Sequence 59, Appl Sequence 32297, A Sequence 28401, A Sequence 79, Appl Sequence 27, Appl Sequence 27, Appl

Sequence Sequence

Sequence

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Sequence

Sequence

Sequence Sequence

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Result Š

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KLOETZER, William S.
NAKAMURA, Takehiko.
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
ANTIBODIES AND USE THEREOF AS THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
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CLASSIFCATION NUMBER: US/09/019,441
FILING DATE: OF-PC-1999
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS,
STREET: P.O. BOX 1404
US-09-972-656-65
US-10-300-675-1
US-09-948-429B-3
US-10-124-807-3
US-10-124-807-3
US-10-124-905-3
US-10-073-138-2
US-10-073-138-2
US-10-077-64-110
US-10-077-632-114467
US-10-309-764-1104
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US-10-309-764-114467
US-10-309-764-114467
US-10-309-764-114467
US-10-309-764-114467
US-09-864-761-32297
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US-10-330-613-27
US-10-330-613-11
US-10-330-613-13
US-10-330-613-39
US-10-330-613-39
US-10-330-530-11
US-10-173-531-23
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REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09019411
Publication No. US20030086921A1
GENERAL INFORMATION:
RAPLICANT: REFF, Mitchell E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (703) 836-
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 35
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Sequence 1, A
Sequence 15,
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Sequence 11,
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Sequence 1,
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366
1 CAGCTGCAGCTGCAGGAGTC......TCCTGGTCACCGTCTCCTCA 366
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1: \( \text{cgn2} \) \( \text{Cptodata} / 2 \) \( \text{pubma} / \text{USO7} \) \( \text{PUBCOMB} \) \( \text{seq} : * \)

2: \( \text{cgn2} \) \( \text{Cptodata} / 2 \) \( \text{pubma} / \text{PCT} \) \( \text{NEW} \) \( \text{PUB. seq} : * \)

2: \( \text{cgn2} \) \( \text{Cptodata} / 2 \) \( \text{pubma} / \text{NEW} \) \( \text{PUB. seq} : * \)

4: \( \text{cgn2} \) \( \text{Cptodata} / 2 \) \( \text{pubma} / \text{NSO} \) \( \text{PUBCOMB} \) \( \text{seq} : * \)

5: \( \text{cgn2} \) \( \text{Cptodata} / 2 \) \( \text{pubma} / \text{NSO} \) \( \text{PUBCOMB} \) \( \text{seq} : * \)

6: \( \text{cgn2} \) \( \text{Cptodata} / 2 \) \( \text{pubma} / \text{NSO} \) \( \text{PUBCOMB} \) \( \text{seq} : * \)

7: \( \text{cgn2} \) \( \text{Cptodata} / 2 \) \( \text{pubma} / \text{NSO} \) \( \text{PUBCOMB} \) \( \text{seq} : * \)

8: \( \text{cgn2} \) \( \text{Cptodata} / 2 \) \( \text{Pubma} / \text{NSO} \) \( \text{PUBCOMB} \) \( \text{seq} : * \)

10: \( \text{cgn2} \) \( \text{Cptodata} / 2 \) \( \text{Pubma} / \text{NSO} \) \( \text{PUBCOMB} \) \( \text{seq} : * \)

11: \( \text{cgn2} \) \( \text{Cptodata} / 2 \) \( \text{Pubma} / \text{USO} \) \( \text{NSW} \) \( \text{PUB} \) \( \text{seq} : * \)

12: \( \text{cgn2} \) \( \text{Cptodata} / 2 \) \( \text{Pubma} / \text{USO} \) \( \text{NSW} \) \( \text{PUB} \) \( \text{Seq} : * \)

13: \( \text{cgn2} \) \( \text{Cptodata} / 2 \) \( \text{Pubma} / \text{USO} \) \( \text{NSW} \) \( \text{PUB} \) \( \text{Seq} : * \)

13: \( \text{cgn2} \) \( \text{Cptodata} / 2 \) \( \text{Pubma} / \text{USO} \) \( \text{PUBCOMB} \) \( \text{Seq} : * \)

14: \( \text{cgn2} \) \( \text{Cptodata} / 2 \) \( \text{Pubma} / \text{USO} \) \( \text{PUBCOMB} \) \( \text{Seq} : * \)

15: \( \text{cgn2} \) \( \text{Cptodata} / 2 \) \( \text{Pubma} / \text{USO} \) \( \text{NBCOMB} \) \( \text{Seq} : * \)

16: \( \text{cgn2} \) \( \text{Cptodata} / 2 \) \( \text{Pubma} / \text{USO} \) \( \text{NBCOMB} \) \( \text{Seq} : * \)

16: \( \text{cgn2} \) \( \text{Cpt
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/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
                                   GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-10-103-686-2
US-10-124-807-11
US-10-291-532-11
US-10-291-532-11
US-10-073-138-6
US-09-905-243-40
US-10-211-357-9
US-10-211-357-9
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US-10-211-357-9
US-09-850-165-15
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
                                                                                                                            using
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Perfect score:
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TITLE OF INVENTION: "MON
TITLE OF INVENTION: TO H
TITLE OF INVENTION: PHAR
TITLE OF INVENTION: PHAR
INTER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
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NAKAMURA, Takehiko
TITLE OF INVENTION: GARMAL ANTI-HUMAN CD23 MONOCLONAL
ANTIBODIES AND USE THEREOF AS THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTG
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 423
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSES: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
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100.0%; Pred. No. 4.5e-104;
ive 0; Mismatches 0;
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APPLICATION NUMBER: US/10/103,686
                                                                                                                                                                                                                                                                                                                    LOCATION: 58.7423
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-019-441-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10103686 Publication No. US20030059424A1 GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
                                                                                                                                        MOLECULE TYPE: DNA (genomic)
FEATURE:
                        LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                   NAME/KEY: mat_peptide
LOCATION: 58..423
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COUNTRY: United States
ZIP: 22313-1404
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                          LOCATION: 1..423
FEATURE:
                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          366; Conservative
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                                                                                                                                                                                                    NAME/KEY:
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US-10-103-686-2
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Best Local
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Anderson, Darrell R.
VENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
VENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
VENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
SQUENCES: 12
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Pred. No. 4.5e-104;
0; Mismatches 0;
                                                                                                                          REFERENCE/DOCKET NUMBER: 012712-353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 11, Application US/09948429B; Patent No. US20020177689A1; GENERAL INFORMATION: Anderson, Darrell R.
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                      mat_peptide
                                                                                                                                                                                                                                               LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                      1..423
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Best Local Similarity 100.0
Matches 366, Conservative
                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
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BURNS, DOANE, SWECKER & MATHIS

ADDRESSEE:

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Sequence 11, Application US/10124807
Publication No. US20030166207A1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF,
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
TORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 256.2; DB 1
Pred. No. 9.2e-70;
0; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFTCATION
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: 08/487,55C
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1431 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 82.2%;
Matches 313; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Teskin, Robin L.
REGISTRATION NUMBER: 3
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LOCATION:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTCTGGTAGTGGTGGGGCCACCAAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACGCGTCCAAGAACCAGTTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACAACCCTCCCTCAAGAGTCAAGTCACCATTCAACAGACACGTCCAAGAACCAGTTC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCCAGAGAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----CGCTAGGCTTCTGGGGCCAGGGA 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCCCAGGGAAGGGGCTGGAGTGGATTTGGGAGTTTCTATAGTAGTAGTAGTGGGAACACCTAC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          358 CGTCTTTTTTCAGTTGTTGGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCGGGA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CAGCTGCAGCTGCAGGAGTCGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 256.2; DB 10; Length Pred. No. 9.2e-70; 0; Mismatches 53; Indels
                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
                                                                                                                                                                                                                                                                                                                                                                                    US 08/487,550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGGCCCAAATAGCTGGAACAA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              346 GTCCTGGTCACCGTCTCCTCA 366
                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teekin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01271
TELECHONE: 703-836-6620
TELEPHONE: 703-836-6221
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                     COUNTY.
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
menty is by Compatible
PC-DOS/MS
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: 699 Prince Street
Alexandria
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82.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1431 base pairs
IYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 70.0
Best Local Similarity 82.2
Matches 313; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                           FILING DATE: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1..1431
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                                                                                                                                                                                                                                                                       FILING DATE
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LOCATION:
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; LOCATION:
US-09-948-429B-11
                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238
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ADDRESSE: BIRNS, DOANE, SWECKER & MATHIS

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

TITLE OF INVENTION: PHARNACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

TITLE OF INVENTION: IMMUNSUPPRESANTS"

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street

CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGIGCAGCIGCAGAGTCGGGCCCAGGACIGGTGAAGCCTTCGGAGACCCTGTCCCT 117
298 TCCCTGAAGCTGAACTCTATGACCGCCGCGGACACGGCCGTGTATTACTGTGTGAGAGAT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC
                                                                                                                           70.0%; Score 256.2; DB 14; Length 1431; 82.2%; Pred. No. 9.2e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 09/383,916
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY AGENT INFORMATION:
NAME: TERKIN, RObin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/124,905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                     346 GTCCTGGTCACCGTCTCTCA 366
                                                                                                                                                                                                                                          GICCIGGICACCGICTCCICA 438
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/10124905; Publication No. US20020166136A1 GENERAL INFORMATION:
                                                                         301 TGGGCCCAAATAGCTGGAACAA
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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EDNESS: not relevant
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Best Local Similarity 82.2
Matches 313; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopby
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
FEATURE:
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; LOCATION:
US-10-124-905-11
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TITLE OF INVENTION: AMEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OR IN
TITLE OF INVENTION: MEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OR IN
TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
FILE REFERENCE: 037003/291872
CURRENT APPLICATION WUMBER: 05/331,187
PRIOR FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 60/331,187
PRIOR FILING DATE: 2001-01-12
PRIOR PAPLICATION NUMBER: 09/758,173
PRIOR FILING DATE: 2001-01-12
PRIOR PELING DATE: 1099-06-26
PRIOR FILING DATE: 1999-06-26
PRIOR FILING DATE: 1999-06-26
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PALENTIN VOYER: 03
SOFTWARE: PALENTIN VOYER: 03
SOFTWARE: PALENTIN VOYER: 03
SOFTWARE: PALENTIN VOYER: 03
SOFTWARE: PALENTIN VOYER: 03
SOFTWARE: PALENTIN VOYER: 03
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SOFTWARE: PALENTIN VOYER: 03
SOFTWARE: PALENTIN VOYER: 03
SOFTWARE: PALENTIN VOXER: 03
SOFTWARE: PALENTIN V
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                                                                                                                                                   301 TGGGCCCAAATAGCTGGAACAA-------CGCTAGGCTTCTGGGGCCAGGGA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
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   TACAACCCTCCCTCAAGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTC 297
                                                                                                       TCCCTGAACCTGAACTCTGTGACCGCGGGGGGCGCGTGTATTACTGTGCCAGAGAT 300
                                                                                                                                                                                                                                                                                                      358 CGTCTTTTTTCAGTTGTTGGAATGGTTTACAACAACAACTGGTTCGATGTCTGGGGCCCGGGA 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13; Length 1431;
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Pred. No. 9.2e-70;
0; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                     346 GTCCTGGTCACCGTCTCCTCA 366
                                                                                                                                                                                                                                                                                                                                                                                                                           418 GrccrggrcAccGrcrcA 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/10291532
Publication No. US20030180290A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HARIHARAN, KANDASAMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.0%;
82.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 82.2
Matches 313; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) NAME/KEY: CDS
; LOCATION: (1)..(1428)
US-10-291-532-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-291-532-11
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Fatent No. US200200620091
Fatent No. US200200620091
Fatent No. US200200620091
Fatent No. US200200620091
FAPPLICATION Alexander H
TITLE OF INVENTION: Monoclonal Antibodies with Reduced
TITLE OF INVENTION: Immunogenicity
FILE REFERENCE: PS0770
CURRENT APPLICATION NUMBER: US/09/905,243
CURRENT FILING DATE: 2001-07-16
FRIOR APPLICATION NUMBER: 09/300,970
FRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 97
SOFTWARE FRATESEQ for Windows Version 3.0
SEQ ID NO 40
                                                                                                                                                                                                                                                                                        53;
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                                                                                                                                                                                                   Query Match 70.0%; Score 256.2; DB 1
Best Local Similarity 82.2%; Pred. No. 9.2e-70;
Matches 313; Conservative 0; Mismatches 53
                                   LOCATION: 1..1431
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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; LOCATION: (1)...(423)
US-09-905-243-40
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                                                                                                                                                                    CCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTCTGGTAGTGGTGGGGCCACCAAC 180
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STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: TIM PC Compatible
COMPUTER: Ploppy disk
SOFTWARE: PatentIn Release #1.0, Version #1.30
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NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-256
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/08/746,361
FILING DATE: 08 NOV-1996
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
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APPLICATION NUMBER: US/10/073,138
FILING DATE: 13-Feb-2002
CLASSIFICATION: <Unknown>
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Publication No. US20020187146A1
GENERAL INPORMATION:
APPLICANT: ANDERSON, Darrell R.
HANNA, Nabil
BRAMS, Peter
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MOLECULE TYPE: DNA (genomic)
PEATURE:
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STRANDEDNESS: single
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APPLICATION NUMBER: US/09/612,914A FILING DATE: 10-Jul-2000 APPLICATION NUMBER: US 08/523,894 FILING DATE: 06-SEP-1995 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/10/211,357
                                                       NAME/KEY: mat_peptide
LOCATION: 1..1404
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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CLASSIFICATION: <Unknown>
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Publication No. US20030077275A1
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
                                                                                                                                                                                                      Query Match 67.2%;
Best Local Similarity 81.4%;
Matches 298; Conservative (
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1..1404
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Newman, Roland A.
Reff, Mitchell B.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
Therapy
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ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/612,914A
FILING DATE: 10-010-2000
APPLICATION NUMBER: US 06/523,894
FILING DATE: 06-5EP-1995
ATTORNEY/AGENT INFORMATION:
NAME: TESKII, ROBIN 1.

REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 31,050
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: RIOPY disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/211,357
FILING DATE: 05-Aug-2002
CLASSIFICATION: <unimage color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of
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TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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Publication No. US20030077275A1
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
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STRANDEDNESS: single
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NAME/KEY:
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US-10-211-357-7
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Reff, Mitchell B.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
Therapy
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Length 1404;
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CORRESPONDENCE ADDRESSE:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PIN PC COMpatible
COMPUTER: PIN PC COMpatible
COMPUTER: PIN PC COMpatible
COMPUTER: PIN PC COMpatible
COMPUTER: PIN PC COMPATIBLE
COMPUTER: PATENTIN Release #1.0, Version #1.30
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Score 246; DB 15;
Pred. No. 1.4e-66;
0; Mismatches 65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NAMBER: US/10/211,357
FILING DATE: 05-Aug-2002
CLASSIFICATION: <university control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of 
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Pred. No. 1.4e-66;
0; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/612,914A
FILING DATE: 10-011-2000
APPLICATION NUMBER: US 08/523,894
FILING DATE: 06-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, ROBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHROMOSOME/SEGMENT: heavy chanton
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TELEPHONE: 703-836-6620
                                                                                                                                           ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
JLE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO: 11:
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Best Local Similarity 81.4%;
Matches 298; Conservative
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CITY: Alexandria
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Newman, Roland A.
Reff, Mitchell B.
TILLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 246; DB 15;
Pred. No. 1.4e-66;
0; Mismatches 65
                                                                                              REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: mat_peptide
LOCATION: 1..1404
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                  REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/10211357
Publication No. US20030077275A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens POSITION IN GENOME:
                                                                                                                                                                                                                                                           TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.2%;
81.4%;
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Best Local Similarity
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NAME/KEY:
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US-10-211-357-11
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301 TGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTC 360
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GENERAL INFORMATION:
APPLICANT: NEWMAN, ROLAND A.
APPLICANT: NEWMAN, ROLAND A.
APPLICANT: HAMNA, NABIL
APPLICANT: RAAB, ROLAND W.
TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
TILLS PREBRENCE: 037003-0286014
CURRENT FILING DATE: 037003-0526014
CURRENT FILING DATE: 1998-05-10
PRIOR FILING DATE: 1998-05-11
PRIOR PILING DATE: 1998-06-07
PRIOR PLING DATE: 1995-04-17
PRIOR APPLICATION NUMBER: 08/397,072
PRIOR PILING DATE: 1995-04-17
PRIOR PILING DATE: 1992-03-23
PRIOR PLING DATE: 1992-03-23
PRIOR PILING DATE: 1991-07-25
NUMBER OF SEQ ID NOS: 114
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Pred. No. 3.5e-66;
0; Mismatches 66
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US-09-905-243-44
IS-09-905-243-44
Sequence 44, Application US/09905243
Patent No. US20020062009A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 81.1%;
Matches 297; Conservative
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; LOCATION: (4)..(420)
US-09-850-165-15
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APPLICANT: Brodin, Thomas N.
APPLICANT: Milson, Do. H.K.
APPLICANT: Obleson, Lennart G.
APPLICANT: Tordsson, M. Jesper
TITLE OF INVENTION: No. US20030176661Alel Antibody with Specificity for Colon Cancer;
TITLE OF INVENTION: No. US20030176661Alel Antibody with Specificity for Colon Cancer;
TITLE OF INVENTION: No. US20030176661Alel Antibody with Specificity for Colon Cancer;
CURRENT APPLICATION NUMBER: US/10/182,132
CURRENT PRICATION NUMBER: PCT/SE01/00395
PRIOR FILING DATE: 2001-02-23
PRIOR FILING DATE: 2000-2-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PARCHIN VET. 2.1
SEQ ID NO 1
LENGTH: 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   389 AGGTGCAGCAGGAGTGGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCA 448
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COGATION: (1)..(747)
OTHER INFORMATION: K293 variable region (scFv); PRT (aa)-sequence OTHER INFORMATION: (1-110), mod Huston (111-129), Vh (130-249)
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Best Local Similarity 83.3%; Pred. No. 2.5e-66;
Matches 304; Conservative 0; Mismatches 55; Indels to
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US-09-850-165-15
; Sequence 15, Application US/09850165
                                                                                                                                                                 ; Sequence 1, Application US/10182132
; Publication No. US20030176661A1
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             366
                                                     415 rccrch 420
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Search completed: December 30, 2003, 03:42:10
Job time : 529.775 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 TCCCCGGGGAAGGGGCTGGAATGGATTGGAAGTTTCTATACTACTACTGGAAATACCTTC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCCTGAACCTGAACTCTGTGACCGCGCGACACGCCGTGTATTACTGTGCCAGAGAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 CAGGTTCAACTACAGGAGTCGGGCCCAGGACTGATGAAGCCTTCGGAGACCCTGTCCCTC 117
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Reff, Mitchell B.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human Therapy
                                                                                                                                                                                                                                                                                                                                                                                                        3,
                                                                                                                                                                                                                                                                                                                                                                  DB 9; Length 420;
                                                                                                                                                                                                                                                                                                                                                                  Score 242.8; DB 9; Length
Pred. No. 1.1e-65;
0; Mismatches 67; Indels
          TITLE OF INVENTION: Monoclonal Antibodies with Reduced
TITLE OF INVENTION: Immunogenicity
FILE REPERENCE: PSO/70
CURRENT APPLICATION NUMBER: US/09/905,243
CURRENT FILING DATE: 2001-07-16
PRIOR PILICATION NUMBER: 09/300,970
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 97
SEQ ID NO 44
LENGTH: 420
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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RADBRESREE: BURNS, DOANE,
STREET: 699 Prince Street
CITY: Alexandria
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Publication No. US20030077275A1
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
Taylor, Alexander H
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.9%;
Matches 296; Conservative
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                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Macaca cynomolgus
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ZIP: 22314-3187
                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (1)...(420)
US-09-905-243-44
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PatentIn Release #1.0, Version #1.30
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Pred. No. 3e-65;
0; Mismatches 66;
                                                                                                                                                                            FILING DATE: 10-311-2000
APPLICATION NUMBER: US 08/523,894
FILING DATE: 06-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTATION NUMBER: 35,030
REJECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 703-836-6620
TELEFRAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 1:
                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/211,357
FILING DATE: OS-Aug-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 420 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 81.0%;
Matches 294; Conservative
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                                                                                                                                                                                     366
1 CAGCTGCAGCTGCAGGAGTC......TCCTGGTCACCGTCTCCTCA 366
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Sequence 5!
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Sequence 4
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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S-08-481-869-19
S-08-476-237-15
3-08-478-039-107
                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .08-545-809A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .09-526-098-11
                                                                                                                                                                                                                                                                                          569978 segs, 220691566 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                OM nucleic - nucleic search, using sw model
                                                                                                                                                                     US-09-019-441-2_COPY_58_423
                                                                                                                                                                                                                                       IDENTITY_NUC Gapop 10.0., Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length
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Sequence 355, App	US-09-042-353-355	ო	404	56.5	206.8	45
Sequence 3, Appli	US-08-793-450-3	4	369	56.8	207.8	44
Sequence 34, Appl	US-08-545-809A-34	m	687	56.9	208.4	43
Sequence 205, App	US-08-758-417A-205	4	403	57.2	209.2	42
	US-09-042-353-357	m	403	57.2	209.2	41
Sequence 23, Appl	US-08-652-816A-23	N	354	57.2	209.5	40
Sequence 3, Appli	US-08-450-363-3	4	357	57.3	209.8	39
Sequence 3, Appli	US-09-014-880-3	~	357	57.3	209.8	38
Sequence 3, Appli	US-09-017-628-3	~	357	57.3	209.8	37
Sequence 3, Appli	US-08-450-578-3	~	357	57.3	209.8	36
'n	US-08-360-125-3	-	357	57.3	209.8	35
Sequence 49, Appl	US-08-477-553A-49	0	384	57.4	210	34
Sequence 31, Appl	US-08-545-809A-31	3	631	58.0	212.4	33
Sequence 13, Appl	US-09-582-337-13	4	450	58.2	213	32
Sequence 20, Appl	US-08-652-816A-20	N	357	58.3	213.2	31
Sequence 1, Appli	US-08-480-774A-1	~	426	59.0	215.8	30
Sequence 50, Appl	US-08-477-553A-50	~	363	59.3	217	5
sednence 4p, Appr	US-08-477-553A-46	7	372	59.5	217.6	28

## ALIGNMEN

US-08-803-085-2

```
Sequence 2, Application US/08803085

Remain No. 6011138

REMERAL INFORMATION:
REPET, Wiltchell E.
APPLICANT: REPET, Wiltchell E.
APPLICANT: RANAWIRA, William S.
APPLICANT: REMET, WILCHELL E.
TITLE OF INVENTION: GAMMA.1 ANTI-HUWAN CD23 WONCCLONAL
TITLE OF INVENTION: GAMMA.1 ANTI-HUWAN CD23 WONCCLONAL
TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
STREET: P.O. BARANALE S.
APPLICANT: VIZINIA
STREET: P.O. BARANALE COMMITS
STREET: P.O. BARANALE COMMITS
STREET: P.O. BARANALE COMMITS
STREET: P.O. BARANALE COMMITS
STREET: P.O. BARANALE COMMITS
STREET: P.O. BARANALE COMMITS
COMPUTER: IMP PC COMPATIBLE COMMITS
STREET: BLEGHTIN RELEASE #1.0, Version #1.30
COMPUTER: IMP COMPATION DATA:
COMPUTER: IMP COMPATION NUMBER: 15.030
STRANET APPLICATION NUMBER: 35.030
TILLSOMWINDER: 15.030
REPERENCE/DOCKET WIMPER: 35.030
TELECOMMUTATION NUMBER: ```

100.0%; Score 366; DB 3; Length 423;

Query Match

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FILING DATE: APPLICATION NUMBER: US 08/487,550 FILING DATE: 07-JUN-1995
  US-09-526-098-11; Sequence 11, Application US/09526098; Patent No. 6492134; GENERAL INFORMATION:
  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
  3: Floppy disk
IBM PC compatible
   70.0%;
   mat peptide
   Conservative
  ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
  1..1431
   CITY: Alexandria
  Query Match
Best Local Similarity
Matches 313; Conserv
   FILING DATE
  ; LOCATION:
; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-487-550-11
   Κ
   STATE: VI
                               NAME/KEY:
  COMPUTER:
  28
   118
  121
  178
   181
   241
  301
   346
  418
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  "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
"MONKEY MONOCLONAL ANTIBODIES SPECIFIC
PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
IMMUNOSUPPRESANTS"
                                    ö
   117
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   CCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCAAC 180
   240
  238 racaacccercercaagagregagrearcarcarricacaagacaccagagaaccagrre 297
   300
  TGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTC 360
   TGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACGTC 417
   178 CCCCCAGGGAAGGGACTGGAGTGGACGTATCTCTGGTAGTGGTGGGGCCACCAAC 237
  298 recercia a cercica a cercica de contra contra contra de contra
   9
   1 CAGCTGCAGCTGCAGGAGTCGGGCCCAAGAGTGGTGAAGCCTTCGGAAGCCCTGTCCCTC
   TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC
  TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGAT
                                    Gaps
                                       ö
                                    Indels
   ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BY SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: O7-JUN-1995
CLASSIFICATION: 435
           Pred. No. 3.5e-101;
                                    ..
0
   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street
CITY: Alexandria
100.0%; Pred. ...
   ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
RGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEPHAX: 703-836-2021
  ; Sequence 11, Application US/08487550
; Patent No. 6113898
   LENGTH: 1431 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
   INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
           Best Local Similarity 100.
Matches 366; Conservative
  TITLE OF INVENTION: "MOD TITLE OF INVENTION: TO ITITLE OF INVENTION: PHAY TITLE OF INVENTION: IMM NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESSE: ADDRESSEE: BURNS, DOA
  TOPOLOGY: linear
MOLECULE TYPE: peptide
   GENERAL INFORMATION:
APPLICANT: Anderson,
  TCCTCA 366
  TCCTCA 423
  USA
   ۲
  RESULT 2
US-08-487-550-11
  STATE: V. COUNTRY:
   358
  361
  121
   418
  181
  241
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APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: PHARMACHENIAL BT.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESCENDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
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   300
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   117
   61 ACCTGCGCTGTCTCTGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
   177
   237
   240
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  358 cercitititadenienegaaneentiacaacaacreeniceareregeeeeeeeea 417
  9
   CCCCCAGGGAAGGGGCTGGATTGGGAGTTTCTATAGTAGTAGTAGAACACCTAC
   CCCCCAGGGAAGGGACTGGATTGGACGTATCTCTCTGGTAGTGGTGGGCCACCAAC
   TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGAT
  298 recercanacricanererandacecececeaneacececercrarracrererendadar
   TGGGCCCAAATAGCTGGAACAA-------CGCTAGGCTTCTGGGGCCAGGGA
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Length 1431;
  Indels
  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
   53;
  DB 3;
  Score 256.2; DB :
Pred, No. 6.7e-68
  0; Mismatches
  OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
  GTCCTGGTCACCGTCTCCTCA 438
   Greenegreacegrerea 366
```

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Sequence 9, Application US/08523894; Patent No. 6136310; GENRRAL INFORMATION: APPLICANT: Hanna, Nabil
   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
  Ouery Match
Best Local Similarity 81.4%;
Matches 298; Conservative (
   LENGTH: 1404 base pairs
  TYPE: nucleic acid
STRANDEDNESS: single
COMPUTER READABLE FORM:
   CHROMOSOME/SEGMENT:
   CHROMOSOME/SEGMENT:
   1..1404
   361 TCCTCA 366
  POSITION IN GENOME
  NAME/KEY:
LOCATION:
  NAME/KEY:
  ;
US-08-523-894-7
   US-08-523-894-9
   181
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  61 ACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
  ACCTGCGCTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGGGCTGGATCCGCCAG 177
  121 CCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTCTGGTAGTGGTGGGGGCCACCAAC 180
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  301 TGGGCCCAAATAGCTGGAACAA-------CGCTAGGCTTCTGGGGCCAGGGA 345
   58 cadericcadericcadadrededececadaacridaradeerrecaadaceriereere 117
  238 TACAACCCCTCCTCAAGAGTCAAGTCACCATTTCAACAGACGGCCCAGAGAACCAGTTC 297
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  358 CGTCTTTTTTCAGTTGTTGGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCGGGA 417
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   Gaps
  US-08-523-894-7
; Sequence 7, Application US/08523894
; Patent No. 6136310
; Patent No. 6136310
; GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
   15;
   Length 1431;
   53; Indels
   DB 4;
   70.0%; Score 256.2; DB 4
82.2%; Pred. No. 6.7e-68;
  3: BURNS, DOANE, SWECKER & MATHIS 699 Prince Street
   0; Mismatches
   418 GTCCTGGTCACCGTCTCTCA 438
   GICCIGGICACCGICICCICA 366
              NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01271
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-620
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1431 base pairs
   TYPE: nucleic acid
STRANDEDNESS: not relevant
 ATTORNEY/AGENT INFORMATION:
  Query Match 70.0
Best Local Similarity 82.2
Matches 313; Conservative
   mat_peptide
   MOLECULE TYPE: peptide
   NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
  1..1431
  linear
   CITY: Alexandria
  RY: USA
22314-3187
  CDS
  ADDRESSEE:
STREET: 699
  NAME/KEY:
LOCATION:
   NAME/KEY:
  TOPOLOGY:
  , LOCATION:
US-09-526-098-11
  STATE: VI
COUNTRY:
ZIP: 2233
  181
   118
   178
  241
   346
   FEATURE
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  61 ACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
   121 CCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGCCCACCAAC 180
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   ---ATATTGAAATATCTTCACTGGTTATTATACTGGGGCCAGGGAGTCCTGGTCACCGTC 414
   58 cadstacadersecadadercedececeadaerregraadeerregadaeeerrerecere 117
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  238 TACAATCCCTCCTCAACAATCGAGTCTCCATTTCAATAGACACGTCCAAGAACCTCTTC 297
  178 TCCCCAGGGAAGGGACTGGAGTGGATCGGCTACATCTATGGCAGTGGTGGGGGCACCAAT 237
   TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC
  Gaps
  ٠,
۳
  heavy chain variable and constant gamma
  Length 1404;
  65; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 06-SEP-1995
CLASSIPICATION: 424
  Score 246; DB 3;
Pred. No. 7.9e-65;
0; Mismatches 65
  ATTORNEY FACENT INFORMATION:
NAME: TESKIN, RObin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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   Gaps
  3;
  GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Hanna, Nabil
APPLICANT: Reff, Mitchell B.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
   Score 246; DB 3; Length 1404;
Pred. No. 7.9e-65;
0; Mismatches 65; Indels
   ORGANISM: Homo sapiens
POSITION IN CENOME:
CHROMOSCOME/SEGMENT: heavy chain gamma 4 with the P and E
CHROMOSOME/SEGMENT: mutation
  ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street
   Sequence 11, Application US/08523894
Patent No. 6136310
   Query Match
Best Local Similarity 81.4%;
Matches 298; Conservative
   LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   1..1404
   linear
   361 TCCTCA 366
   415 TCCTCA 420
   CITY: Alexandria
  TOPOLOGY: line
MOLECULE TYPE: D
ORIGINAL SOURCE:
  NAME/KEY:
LOCATION:
  NAME/KEY:
LOCATION:
  US-08-523-894-11
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   61 ACCTGCGCTGTCTCTGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
   TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC 240
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  Gaps
  3,
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
   CHROMOSOME/SEGMENT: heavy chain gamma 4 with the E mutation
  Length 1404;
  65; Indels
  STATE: VA

CUUNTRY: USA

ZIP: 22314-3187

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIPICATION: 424
ATTONEY/AGENT INFORMATION:
NAME: TERRYNCE/DOCKET NUMBER: 35,030
REFERRNCE/DOCKET NUMBER: 35,030
REFERRNCE/DOCKET NUMBER: 35,030
TELECOMMUNICATION INFORMATION:
TELEPAK: 703-836-6620
ITELEPAK: 703-836-620
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
DEMOTTH: 1404 base pairs
  Score 246; DB 3;
Pred. No. 7.9e-65;
   0; Mismatches
   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
  67.2%;
  ORGANISM: Homo sapiens POSITION IN GENOME:
  Query Match
Best Local Similarity 81.4
Matches 298; Conservative
  mat_peptide
  single
   TYPE: nucleic acid
STRANDEDNESS: singl
  1..1404
   NAME/KEY:
LOCATION:
   NAME/KEY:
LOCATION:
   US-08-523-894-9
   181
   241
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Query Match

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  181 TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC 240
   TCCCTGAACCTGAACTCTGTGACCGCCGCGCACACGCCCGTGTATTACTGTGCCAGAGAT 300
  301 TGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTC 360
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  358 ---ATATTGAAATATCTTCACTGGTTATTATACTGGGGCCAGGGAGTCCTGGTCACGTC 414
  APPLICANT: HANNA, Nabil
APPLICANT: RAAB, Ronald W.
TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
  CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,072A
FILING DATE: 25-JAN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION NUMBER: US 07/735,064
   ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria STATE: Virginia STATE: Virginia STATE: Virginia STATE: Virginia COUNTRY: United States ZIB: Z1313-1404
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: Patentin Release #1.0, Version #1.
  012712-067
  Sequence 19, Application US/08379072A Patent No. 5658570 GENERAL INFORMATION:
   TILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa Stanek
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELECHONE: (703) 836-6620
   APPLICANT: NEWMAN, Roland A.
   DNA (genomic)
   TELEFAX: (703) 836-2021 INFORMATION FOR SEQ ID NO:
  361 TCCTCA 366
  TCCTCA 420
   linear
  STRANDEDNESS
   -08-379-072A-19
   US-08-379-072A-19
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120
   300
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  121 CCCCCAGGGAAGGGACTGGAGTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAAC 180
   240
   240
  300
  TCCCTGAAACTGAGGTCTGTGACCGCCGCGACACGGCCGTCTATTACTGTGCGAGTAAT 360
   61 cadericcaderideaddaddddddddddaddcrigaadcerreddaddcerererere 120
   ---ATATTGAAATATCTTCACTGGTTATTATACTGGGGCCAGGGAGTCCTGGTCACCGTC 417
  9
  61 ACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG
   121 Accrecaerereregreseres reaces es acraramentarios receses es accrecaeres es ac
   TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC
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  Sequence 19, Application US/08481869
Patent No. 5693780
GENERAL INFORMATION:
APPLICANT: NEWAN, Roland A.
APPLICANT: RAMB, Rohald W.
TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
NUMBER OF ENURINGS 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
  ٠<u>.</u>
   Indels
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/08/481,869
Pred. No. 1.6e-64;
0; Mismatches 66
  REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 012712-067
  US/08/379,072A
   PILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UNBER: US/08/379,0728
FILING DATE: 25-JAN-1995
APPLICATION NUMBER: US 07/912,292
  FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
  US 07/735,064
81.18;
   FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
  NAME: Rea, Teresa Stanek
  STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
Best Local Similarity 81.1
Matches 297; Conservative
  APPLICATION NUMBER:
  TCCTCA 423
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   361
  418
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PRIOR APPLICATION DATE: 23-FARATISTE PRIOR APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-UTL-1991
ATTORNEY AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE FOOCKET NUMBER: 012712-133
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION S36-6620
TELEPHONE: (703) 836-620
TELEPHONE: (703) 836-2021
SEQUENCE CHARACTERISTICS:
   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
   LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   361 TCCTCA 366
   RESULT 10
US-08-478-039-107
   US-08-476-237-15
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  301 TGGGCCCAAATAGCTGGAACGAACGCTAGGCTTCTGGGGCCCAGGGAGTCCTGGTCACGGTC 360
   61 caderideadecrecadeadecededecedadacerecadadecerredadadecererere 120
   61 ACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
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  Gaps
  Sequence 15, Application US/08476237

Patent No. 5756096

GENERAL INFORMATION

APPLICANT: NEWMAN, Roland A. APPLICANT: HANNA, Nabil

APPLICANT: RAMB, Ronald W. APPLICANT: RAMB, Ronald W. APPLICANT: RAMB, Ronald W. APPLICANT: RAMB, Ronald W. APPLICANT: RAMB, Ronald W. APPLICANT: RAMB, ROMBRESSE: 16

CORRESPONDENCE ADDRESS:

ADDRESSE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404

CITY: ALexandria

COUNTRY: United States

ZIP: 22131-1404

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COMPUTER: IBM CC Compatible

COMPUTER: BATHIG SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: Release #1.0, Version #1.30
  Length 423;
   66; Indels
  DB 1;
  Query Match 66.8%; Score 244.4; DB 1
Best Local Similarity 81.1%; Pred. No. 1.6e-64;
Matches 297; Conservative 0; Mismatches 66
   APPLICATION NUMBER: US/08/476,237
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
                TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TELECOMMUNICATION INFORMATION:
  CURRENT APPLICATION DATA
   TCCTCA 366
   TCCTCA 423
  RESULT 9
US-08-476-237-15
  ;
US-08-481-869-19
  121
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121 CCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAAC 180
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   361 --- ATATTGAAATATCTTCACTGGTÄTTATACTGGGGCCAGGGAGTCCTGGTCACGTC 417
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   TCCCTGAACCTGAACTCTGTGACCGCCGCGCACACGGCCGTGTATTACTGTGCCAGAGAT 300
  301 recerciala acresia de de cercica de contra
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  TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC
  1 CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC
   Gaps
   <u>ب</u>
   Sequence 107, Application US/08478039
Patent No. 5681722
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Hanna, Nabil
APPLICANT: Hanna, Nabil
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
        Length 423;
   Indels
        DB 1;
   99
   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince St. CITY: Alexandria STATE: WAS COUNTRY: USA COUNTRY: USA COUNTRY: BASABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
Query Match 66.8%; Score 244.4; DB 1
Best Local Similarity 81.1%; Pred. No. 1.6e-64;
Matches 297; Conservative 0; Mismatches 66
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418 TCC 420

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PatentIn Release #1.0, Version #1.30

PC-DOS/MS-DOS

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  3;
  APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Hanna, Nabil
APPLICANT: Hanna, Nabil
TITLE OF INTRATION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPENDENCE ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
  Length 420;
  Indels
   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
  Query Match 66.0%; Score 241.4; DB 1; Best Local Similarity 81.0%; Pred. No. 1.3e-63; Matches 294; Conservative 0; Mismatches 66;
  APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
RICAR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
RICAR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
  APPLICATION NUMBER: US/08/476,349A
FILING DATE: 07-JUN-1995
   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
  Sequence 107, Application US/08476349A
Patent No. 5750105
GENERAL INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   POSITION IN GENOME:
CHROMOSOME/SEGMENT: Anti-CD4 VH
   NAME: FEEKIN EGG., RODIN L. REGISTRATION NUMBER: 35,030 REFERENCE/DOCKET NUMBER: 01 TELECOMMUNICATION INFORMATION: 703-836-6620
   TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
  nucleic acid
BDNESS: not relevant
GY: not relevant
  420 base pairs
  NAME/KEY: mat_peptide
LOCATION: 61..420
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  66.0%; Score 241.4; DB 1; Length 420; 81.0%; Pred. No. 1.3e-63;
  66; Indels
   PILING DATE: 0.-con------
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 2-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 0.-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 0.-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 2-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq.; Robin L.
NAME: Teskin Esq.; Robin L.
REGISTRATION NUMBER: 012712-160
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRANCE ASO D NO: 107: SEQUENCE CHARACTERISTICS:
LUMPORMATION FOR SEQ ID NO: 107: SEQUENCE CHARACTERISTICS:
LYPE: nucleic acid
TYPE: nucleic acid
  0; Mismatches
SOFTWARE: PRICELLATON DATA:
CURRENT APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995
  CHROMOSOME/SEGMENT: Anti-CD4 VH
  TOPOLOGY: not relevant LEGHT. TOTOLOGY:
   Matches 294; Conservative
   mat_peptide
61..420
  MOLECULE TYPE: peptide ORIGINAL SOURCE:
  Similarity
   4..420
  ORGANISM: Monkey
   POSITION IN GENOME
   NAME/KEY:
LOCATION:
   ; NAME/KEY:
; LOCATION:
US-08-478-039-107
   181
   121
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   Query Match
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   121 Accrecasrercricresrescrecareacesreacrarrarresrreresreceeded 180
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  APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5767246ihiko ITO
APPLICANT: No. 5767246ihiko ITO
APPLICANT: Razuhiro NAGAKB
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoch, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
  .;
:
  Length 420;
  Indels
   Score 241.4; DB 3;
Pred. No. 1.3e-63;
0; Mismatches 66;
   ZIP: 20005
COMPUTER READABLE FORM:
WEDLUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
   FILING DATE:
CLASSIPFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
  US-08-360-125-9; Sequence 9, Application US/08360125; Patent No. 5767246
  66.0%;
81.0%;
  APPLICANT: Saiko HOSOKAWA APPLICANT: TOShiaki TAGAWA
   Best Local Similarity 81.0
Matches 294; Conservative
  mat_peptide 61..420
   4..420
  CITY: Washington STATE: D.C.
   GENERAL INFORMATION:
  U.S.A.
  TCC 363
   418 TCC 420
                                   NAME/KEY:
LOCATION:
FEATURE:
  NAME/KEY:
LOCATION:
   COUNTRY:
   US-08-523-894-1
   181
   241
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   Query Match
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   181 recechégénhégénérhégheghregernenterregenegegégégégénén 240
  TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC 240
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   ACCTGCGCTGTCTCTGGTGGCTCTCTCTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
   Accrecasoricricios de descritos de la contra del la contra della contr
   CCCCCAGGGAAGGGACTGGAGTGGACGTATCTCTGGTAGTGGTGGGGCCACCAAC 180
  TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGAT 300
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  361 ---ATATTGAAATATCTTCACTGGTAATATATACTGGGGCCAGGGAGTCCTGGTCACCGTC 417
   GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Newman, Roland A.
APPLICANT: Neff, Witchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
STREET: 699 Prince Street
CITY: Alexandria
   ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: light variable domain of CE9.1
  COUNTRY: USA
ZIP: 22314-3187
COMPUTER READBLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILLING DATE: 06-SEP-1995
CLASSIFICATION: 424
  US-08-523-894-1
; Sequence 1, Application US/08523894
; Patent No. 6136310
  ATTORNEY JELALINE 12.2
ATTORNEY JEBNIN 10.2
NAME: TEEKIN, RODIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEFRON: 703-836-620
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTER STICS:
LENGTH: 420 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   ACLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
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   STATE:
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Cancer

240

180

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Sequence 9, Application US/08450578

Patent No. 5837845

GENERAL INFORMATION:
APPLICANT: Salvo HOSOKAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: Voko HIRAKAWA
APPLICANT: No. 58378451inko ITO
APPLICANT: No. 58378451inko ITO
APPLICANT: No. 58378451inko ITO
APPLICANT: No. 58378451inko ITO
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APPL
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178 AACTACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAG 237
   238 TICTCCCTGAACCTGAACTCTGTGACGCGCGGGACACGGCCGTGTATTACTGTGCCAGA 297
   298 GATTGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCCAGGGAGTCCTGGTCACC 357
  MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible OPERATING SYSTEM: MS.DOS SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/450,578 FILING DATE: MAY 25, 1995 CLASSIFICATION NUMBER: 08/360,125 PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/360,125 FILING DATE: December 20, 1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/905,534 FILING DATE: June 29, 1992 ATTORNEY/AGENT INFORMATION: NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REGISTRATION NUMBER: 33,367 REGISTRATION NUMBER: 33,367 REGISTRATION NUMBER: MATTEN NUMBER: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:
   SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
   STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
  INFORMATION FOR SEQ ID NO:
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CITY: Washington
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  FRAGMENT TYPE:
ORIGINAL SOURCE
   MOLECULE TYPE:
   RESULT 14
US-08-450-578-9
   ANTI-SENSE:
   TELEFAX:
  셤
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  61 ACCTGCGCTGTCTCTGTGGCTCTGTCAGCAGTAGTA---ACTGGTGGACCTGGATCCGC 117
   61 Accrecacrerereresegencearcascastastastastracrasseseresarecee 120
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  CELL TYPE: Hybridoma producing human antibody 1-3-1 CELL LINE: ORGANELLE: IMMEDIATE SOURCE: LIBRARY:
  FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
  NAME: Waren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
   FILING DATE: June 29, 1992 APPLICATION NUMBER:
   FILING DATE:
ATTORNEY/AGENT INFORMATION:
   INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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HYPOTHETICAL:
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NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
  CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
   STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
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ORIGINAL SOURCE:
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   ANTI-SENSE:
   JOURNAL:
VOLUME:
  TELEFAX:
   US-08-360-125-9
   UNITS:
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Search completed: December 29, 2003, 21:48:28 Job time : 41.2876 secs
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   Grerectea 366
   TYPE: DNA
ORGANISM: Unknown
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CELL TYPE:
CELL TYPE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
CHONEN:
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-9
   UNITS:
FEATURE:
INAME/KES:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
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  118
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  238
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RESULT 15
US-09-017-628-9
; Sequence 9, Application US/09017628
; Patent No. 5990287
; GENERAL INFORMATION:
; APPLICANT: HOSOKAWA, Saiko

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  298 degadetracegegetractacegraficadestéricadechadegaceacégicade 357
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APPLICANT: HIRAKAWA, YOKO
APPLICANT: HIRAKAWA, YOKO
APPLICANT: HIRAKAWA, YOKO
APPLICANT: HIRAKAWA, YOKO
APPLICANT: NAGAIKE, Kazuhiro
TITLE OF INVENTION: HUWANA MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
TITLE OF INVENTION: HUWARR: US/09/017,628
FILE REFERENCE: 177/527361KH
CURRENT APPLICATION NUMBER: US/09/017,628
CURRENT APPLICATION NUMBER: US/09/017,628
CURRENT FILING DATE: 1998-02-02
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PATENTIN VOICE: 2.0
SOFTWARE: PATENTIN VOICE: 2.0
SOFTWARE: PATENTIN VOICE: 2.0
SEQ ID NO 9
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Matches 301; Conservative 0; Mismatches 62; Indels 6
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, OTHER INFORMATION: Hybridoma producing human antibody 1-3-1
US-09-017-628-9
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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| OM nucleic - nu                       | nucleic                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | search, using sw model                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |            |
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| Run on:                               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | December 29, 2003, 16:08:50 ; Search time 1466.44 Seconds (without alignments) 9875.644 Million cell updates/sec                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | s<br>/ sec |
| Title:<br>Perfect score:<br>Sequence: | US-09<br>354<br>1 GA(                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | US-09-019-441-4_COPY_S8_411<br>354<br>1 GAGGIGCAGCIGGIGGAGICTCCIGGICACCGICICCICA 35                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |            |
| Scoring table:                        | IDENTI<br>Gapop                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | IDENTITY NUC<br>Gapop 10.0 , Gapext 1.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | ·          |
| Searched:                             | 2888711                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 711 segs, 20454813386 residues                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |            |
| Total number of                       | hits                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | satisfying chosen parameters: 5777422                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |            |
| Minimum DB seq<br>Maximum DB seq      | length:<br>length:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | h: 0<br>h: 2000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |            |
| Post-processing:                      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Minimum Match 0%<br>Maximum Match 100%<br>Listing first 45 summaries                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |            |
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Pred. No. is the number of results predicted by chance to have a

|            |       | ,          |            |          | SUMMARIES |                         |
|------------|-------|------------|------------|----------|-----------|-------------------------|
|            | Ö     | ery<br>tch | Length     | DB       | QI        | cription                |
|            | 1 10  | 5.5        | 19040      | 1        | BD075127  |                         |
| 7          | 255.2 | 72.1       | 9          | 0        | 73        | 920 Macaca              |
| e          | 54.   | ä          | 9          | σ        | 7391      | 3919 Macaca             |
| 4          | 25    | ;          | 9          | σ,       | 7391      | 3918 Macaca             |
| ហ          | 52.   | ή.         | S          | σ        | 332       | 6355 Papio              |
| <b>9</b>   | 20.   | · ·        | S)         | 9        | _         | 5540 Human              |
| 7          | 20.   |            | 458        | 9 (      | BD094918  | JIB Human m             |
| <b>∞</b> ( | 246.6 | ٠.<br>د    | 462        | <i>a</i> | ~· •      | AFI/3921 Macaca mu      |
| י<br>א כ   | 4 0   |            | 414        | א ע      |           | 707                     |
| 1 1        | 777   | o a        | 264        | ט ע      | BD167727  | 61700 Mecin             |
| 12         | 4 4   | . a        | 448        | σ        |           | 673                     |
|            | . 6   | . α        | 44.0       | , σ      | 1100491   | Human                   |
| 14         | 42.   |            | 429        | 6        | HSHA3D11G |                         |
|            | 42.   | 8          | 667        | σ        | HSU03894  | U03894 Human rheum      |
| 16         | 41.   | œ.         | 462        | 6        | AF173923  | $\overline{\mathbf{c}}$ |
| 17         | 41.   | . 60       | 714        | σ        | HSA6111   | 11                      |
| 18         |       | 8          | 714        | σ        | HSA6115   | 5 Homo                  |
| 19         | 41.   | 6          | 714        | 0        | HSA6117   | Ношо                    |
| 20         | 41.   | œ.         | 714        | σ,       | HSA6118   | Homo                    |
| 21         | ♥ .   |            | 714        | σ (      | HSA6114   | Homo                    |
| 22         | 4     | ۲.         | 714        | σ,       | -         | Homo sa                 |
| 23         | ₩,    | ٠.         | 720        | 9 1      | AX740176  | Sequenc                 |
| 4.1        | 42.0  | ٠.         | 027        | ه م      | BD0//368  | Mechoa                  |
| 2 7        | 7 c   | ٠.         | 4. u       | ט כ      | HUMIGHADC | uman 1                  |
| 9 0        | 238.6 | ٠,         | 540<br>575 | ם מ      | 0 5       |                         |
| 28         | . 6   |            | 3 6 6      | Ŋο       | HUMIGHVAB | L06101 Homo sapien      |
| 50         | 38    |            | 462        | σ        | ~1        |                         |
| 30         | 38.   | _          | 714        | 6        | 16        |                         |
| 31         | 37    | 7          | 348        | σ        | AB021526  | Homo                    |
| 32         | 37    | 7          | 348        | σ        | HSIGHADI3 | X98751 H.sapiens        |
| 33         | 37    | 7          | 372        | σ        | ٠.        | 5 H.sapie               |
| 34         | 37    | 7          | 376        | σ        | AF115108  | m                       |
| 35         | 237   | Ġ          | 742        | 9        | BD161779  | 779 Metho               |
| 36         | 7     | Ġ          | 742        | 9        | BD167726  | BD167726 High effi      |
| 37         | 236.2 | ů.         | 437        | თ        | 5         | 113 Human               |
| 38         | 236   | ů.         | 348        | σ        | 20        | 50 Human                |
| 39         | 236   | Ġ          | 360        | σ        | HSA239363 | 239363 Ношо ва          |
|            | 236   | ů          | 360        | σ        | >         | 5898 Homo sapi          |
|            | 236   | Ġ          | 527        | σ        | Н         | 8716 Homo               |
| 42         | N     | Ġ          | 534        | σ        | 7         | 1 Homo sa               |
|            | 235.8 | 9.99       | 376        | თ        | AF115107  | 115107 Homo sa          |
| 44         | 35.   | 9          | 342        | σ        | 8         | B06698                  |
|            |       |            |            |          |           |                         |

ALIGNMENTS

|          |          | linear PAT 27-AUG-2002 | cells                                                             | he                                                             |       |           |                        |                    |              |              |               |                      |             | cells                                                             |   |
|----------|----------|------------------------|-------------------------------------------------------------------|----------------------------------------------------------------|-------|-----------|------------------------|--------------------|--------------|--------------|---------------|----------------------|-------------|-------------------------------------------------------------------|---|
|          |          | T 27-P                 | alian                                                             | shing t                                                        |       |           |                        |                    |              |              |               |                      |             | alian                                                             |   |
|          |          | ΡŹ                     | mamu                                                              | mplie                                                          |       |           |                        |                    |              |              |               |                      |             | mam                                                               |   |
|          |          | ear                    | in                                                                | Ö                                                              |       |           |                        |                    |              |              |               |                      |             | in                                                                |   |
|          |          | lin                    | sites                                                             | for a                                                          |       |           |                        |                    |              |              |               |                      | ٠ <u>.</u>  | sites                                                             |   |
|          |          | 19040 bp DNA           | Method for integrating genes at specific sites in mammalian cells | via homologous recombination and vectors for accomplishing the |       |           |                        |                    |              |              |               |                      | chlan, K. I | Method for integrating genes at specific sites in mammalian cells |   |
|          |          | ď                      | at                                                                | and                                                            |       |           |                        |                    |              |              |               |                      | clac        | at                                                                |   |
|          |          | 19040                  | genes                                                             | ation                                                          |       |           |                        |                    |              |              |               |                      | and M       | genes                                                             |   |
|          |          |                        | ing                                                               | mbin                                                           |       |           | 20730                  |                    |              |              |               | (01                  | R.S.        | ing                                                               |   |
|          |          |                        | egrat                                                             | reco                                                           |       |           | BD075127.1 GI:22620730 | JP 2001516221-A/3. |              |              |               | 1 (bases 1 to 19040) | nett,       | egrat                                                             |   |
|          |          |                        | int                                                               | goog                                                           |       |           | B                      | 221-               | g            | 껗            | g             | 1<br>2               | Bar         | int                                                               |   |
|          |          | 7                      | for                                                               | 010                                                            |       | 7         | 7.1                    | 516                | 1,61         | ifi          | ifi           | 68                   | Ξ.          | for                                                               |   |
|          |          | BD075127               | poq                                                               | hor                                                            | o)    | BD075127. | 7512                   | 2001               | unidentified | unidentified | unclassified. | (bas                 | £,¤.        | poq                                                               |   |
|          |          | BDO                    | Met                                                               | via                                                            | same. | BDO       | BDO                    | ц                  | uni          | uni          | nuc           | _                    | Ref         | Met                                                               |   |
| -        | 27       |                        | TION                                                              |                                                                |       | NOI       | z                      | DS;                |              | NISM         |               | NCE                  | ORS         | ϫ                                                                 |   |
| KESOLT I | BD075127 | LOCUS                  | DEFINITION                                                        |                                                                |       | ACCESSION | VERSION                | KEYWORDS;          | SOURCE       | ORGANISM     |               | REFERENCE            | AUTHORS     | TITLE                                                             | - |
| ¥        | В        | П                      | Δ                                                                 |                                                                |       | Þ         | >                      | ×                  | S            |              |               | æ                    |             |                                                                   |   |

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Germline repertoire of the immunoglobulin V(H)3 family in rhesus
   10912503
  103
                    monkeys
   misc_feature
  61
   121
  181
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   source
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AUTHORS
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PUBMED
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JOURNAL
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   9
  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria; Primates; Catarrhini, Cercopithecidae; Cercopithecinae, Macaca.

(Crangithecinae, Macaca.

Helmuth, E.P., Letvin, N.L. and Margolin, D.H.
   MITCHELL B REFF.RICHARD SPRNCE BARNETT, KAREN RETTA MCLACHLAND PC C12N15/90, C12N15/95, C12Q1/68, C12N5/10, C12N15/13, PC C07K16/28, PC C12N15/12, C07K14/705, G01N33/53, C12N15/62, C07K19/00 CC Strandedness: Single; CC Topology: Linear; CC Method for integrating genes at specific sites in mammalian CC homologous recombination.
   via homologous recombination and vectors for accomplishing the Patent: JP 2001516221-A 3 25-SEP-2001;
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25-SEP-2001
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   tch 95.5%; al Similarity 98.9%; 351; Conservative (
  /db_xre_
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   Macaca mulatta
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KEYWORDS
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   DEFINITION
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AUTHORS
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  Margolin, D. H.
Direct Submission
Submitted (02-AUG-1999) Viral Pathogenesis Division, Beth Israel
Deaconess Medical Center, Research East 113, PO Box 15732, Boston,
  9
  ij
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   Submitted (02-AUG-1999) Viral Pathogenesis Division, Beth Israel Deaconess Medical Center, Research East 113, PO Box 15732, Boston, MA 02215, USA
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CTGTATCTTCAAATGGACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAG 453
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Helmuth, B.F., Letvin, N.L. and Margolin, D.H.
Germline repertoire of the immunoglobulin V(H)3 family in rhesus
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Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
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Germline repertoire of the immunoglobulin V(H)3 family in rhesus
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  GAGGTGCAGCTGGAGGTCTGGGGGGCGCTTGGCAAAGCCTGGGGGGCCCTCAAGACCCTGGAACTC
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458 bp DNA linear PAT 27-AUG-2002 Human monoclonal antibody against TGF-beta-II receptor and medicinal use thereof.
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1 (basea 1 to 458)
Sakamoto,S. and Kamada,M.
Human monoclonal antibody against TGF-beta-II receptor and mandicinal use thereof patent: JP 2001206899-A 2 31-JUL-2001;
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08-NOV-2000 JP 2000340216
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Cercopithecinae; Papio.

1 (bases 1 to 429)

Scinicariello, F., Jayashankar, L. and Attanasio, R. Baboon immunoglobulin variable region heavy chains: identification of genes homologous to members of the human IGHVI-IGHV7 subgroups Ilmmunogenetics 53 (10-11), 815-820 (2002)
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Direct Submission
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Sakamoto, S. and Kamada, M.
Human monoclonal antibody for human TGF-beta type II receptor and
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I SAKAMOTO, MASATUMI KAMADA
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Direct Submission
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Catarrhini; Cercopithecidae;
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  Design and use of a phage display library. Human antibodies with subnanomolar affinity against a marker of angiogenesis eluted from a two-dimensional gel J. Biol. Chem. 273 (34), 21769-21776 (1998) 98371014
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Submitted (12-MAY-1998) Viti F., Molecular Biology and Biophysics,
ETH (Swiss Federal Institute of Technology), ETH Hoenggerberg,
CH-8093 Zuerich, SWITZERLAND
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  Method
   Kaneko, K.
Method for screening high-efficiency antibody
Patent. JP 2002174635-A 164 21-JUN-2002.
JAPAN SCIENCE AND TECHNOLOGY CORP, PRESIDENT OF NATIONAL CENTER
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PP 21-JUN-2002
PP 07-DEC-2000 JP 2000373259
PI KIYOTOSHI KANEKO 9, C12221/08, C1201/68, C12N15/00 CC for screening high-efficiency antibody FH Key Location/Qualifiers
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Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
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URL:http://www.fujita-hu.ac.jp/immunity/.
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  High efficiency screening method for antibodies
Patent: WO 0242774-A 164 30-MAY-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP, JAPAN AS REPRESENTED BY
PRESIDENT O KAZUHIKO KATAYAMA PSACHIATRY MINISTRY OF HEALTH LABOUR
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Huang, C. and Stollar, B.D.

A majority of 19 H chain cDNA of normal human adult blood

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Stollar, B.D.
Direct Submission
Submitted (10-AUG-1993) Stollar B.D., Tufts University,
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Generic analysis of self-associating immunoglobulin G rheumatoid factors from two rheumatoid synovia implicates an antigen-driven
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La Jolla, California
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Match Length DB
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1201
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em gss i
  em gas
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67.6
67.6
66.6
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BP 191 91006 EVRY cedex - France
BM 11: seqref@genoscope.cns.fr. Web : www.genoscope.cns.fr
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more information about this cluster, see
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BX417408 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE009Y115
5-PRIME, mRNA sequence.
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more information about this cluster, see
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603616742F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5440475 5',
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

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   1 GAGGTGCAGCTGGTGGAGTCTGGGGGGGGCTTGGCAAAGCCTGGGGGGGTCCCTGAGACTC
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   NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODE009AE08QP1. Location/Qualifiers
  Gaps
   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can k
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM1913 row: d column: 12
  301 TTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 354
   489 geággganaciginangiácigatóraggichadogachacidercigitárichacida 542
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Pred. No. 1.8e-51;
0; Mismatches 58; Indels 6;
   40 others
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   Contact: Robert Strausberg, Ph.D.
   324 9
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81.9%;
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  Unpublished
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   295 TACTACGCAGACTCAGTGAAGGCCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCA 354
  CIGITICITCAAAIGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAG- 299
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  9
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I thasea I to 447noi.nih.gov/. NHF-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
   471
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  Email: cgapbs-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

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Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
  AW402613
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   95 GAĞĞTĞCAĞTTĞĞTĞĞAĞTCTĞĞĞĞGAĞĞCCTĞĞTCAAĞCCTĞĞĞĞĞĞTĞCCCTĞAĞAĞTC 154
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  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
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IMAGE:3055710 5', mRNA sequence.
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   CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
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  CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
   CTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTTATTACTGTGCGAGA 364
   351
  crcaaragragaageracrrrrrraacracragageccagagaacccragreaccercic 424
   9
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
   TTCTACGCAGACTCTGTGAAGGGCCGATTCACCATCTCCCAGAGACAACGCCAAGAACTCA
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DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbp/image/image.html
Seq primer: M13 Forward.
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   Score 231.4; DB 9
Pred. No. 1.4e-49;
0; Mismatches 51
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Matches 298; (
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   BASE COUNT
ORIGIN
   REFERENCE
AUTHORS
TITLE
JOURNAL
   RESULT 9
AW401428
   FEATURES
   COMMENT
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   TGGTACGCAGACTCCGTGAAGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACAC
  TCCTGTGCAGCCTCTG-----GATTCACCTTCAGTAGCGATAGCATGAACTGGGTCCGC 189
   CAGGCTCCAGGGCCAGGGCCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
   190 CAGGCTCCAGGCAAGGGGCTGGAGTGGGTCTCATCCATTAGTAGTAGTAGTTCATA 249
   250 TACTACGCAGACTCAGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCA 309
   CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCG--- 297
  310 CTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGA 369
  ------AGCTTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACC 345
   370 GCCCATAGTAGCAGCTGGCCACGCACGACTGACTACTGGGGGCCAGGGAACCCTGGTCACC 429
  1 GAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
   þe
   Gaps
                 Email: cgapbs.remail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staddt, M.D., Ph.D.

TISSUE Procurement: Louis M. Stadt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can I

Clone distribution: MGC clone distribution information can I

Cloud through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: MM3 Forward.
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Robert Strausberg, Ph.D.
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  346 GTCTCCTCA 354
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  Similarity
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  BF97477
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ORIGIN
  DEFINITION
  SOURCE
ORGANISM
  ACCESSION
   VERSION
KEYWORDS
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   FEATURES
COMMENT
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/tissue_type="primary B-cells from tonsils (cell line)"
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/clone lib="NHH MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXAhoI sites using the
following 5' adaptor: GGACAGGG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
Callifornia, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
1 others
  235
  181
   121
  236 AGGCTCCAGGGAAGGGGCTGGAGTGGGTTTCATACATTAGTAGTAGTAGTATATACTACACA 295
  241
  296 GCTACGCAGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACGCCAAGAACTCAC 355
   AGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCCACGTATTAGTAGTAGTGGTGATCCCACAT 181
  242 TGTTTCTTCAAATGAACAGCCTGAGAGCTGACGACACGGCTGTCTATTACTGTGCGAG-- 299
  ------CTTGACTACAGGTCTGACTCCTGGGCCCAGGGAGTCCTGGTCACCG 346
   Craniata; Vertebrata; Buteleostomi;
Catarrhini; Hominidae; Homo.
   Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llhi.gov

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High quality sequence stop: 696.
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   182 cerenecadecrere-----garreacereagadracracardaderegece
  AGGTGCAGCTGGTGGAGTCTGGGGGGGCTTGGCAAAGCCTGGGGGGGTCCCTGAGACTCT
  GGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCC
  182 GGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACA
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National Institutes of Health, Mammalian Gene Collection (MGC)
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AUTHORS
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JOURNAL
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(0.5-1: Ekb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
AW401428 16-FEB-2000 UL-HF-BKO-aad-b-02-0-UI.rl NIH MGC_36 Homo sapiens CDNA clone IMAGE:3053139 5', mRNA sequence.
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  348
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  195
   CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
  crerarcrecaeareacaecreaeaecceaeaeacaececrererrarracreredeaea 375
   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 443)
   CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCCATGAGTAGTACTAGTACTACATA
  Email: cgapbs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward.
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   TACTACGCAGACTCAGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCCAAGAACTCA
  301 TTGACTACAGGG-----TCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTC
  376 GGAGTTCCCATGGTTCAGTTCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACGTC
  11 (Jacks L. C. 173)
Marional Institutes of Health, Mammalian Gene Collection (MGC)
  Gaps
  18;
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   Homo sapiens
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TITLE
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KEYWORDS
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   COMMENT
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AW401386 S82 bp mRNA linear EST 16-FEB-2000
UI-HF-BKO-aau-h-03-0-UI.rl NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3055324 5', mRNA sequence.
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  61 TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 120
  CAGGCTCCAGGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
  racracecaeacrerereaadeeceerreacearereeaeaeaeaeaeaeceaaeaeaecee 365
   CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCG--- 297
  191
   9
   Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Sass) to 582)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
   Contract: Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Bco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: Ml3 Forward.
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ò 셤

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John Total Barbards Site 1: EcoRI; genotype Al7; Total Note="Vector: pGEM-T; Site 1: EcoRI; genotype Al7; Total Not was isolated from rootle harvested 6 days after inoculation with Aphanomyces euteiches zoospores. CDNA was prepared from total RNA using the SMART FCR CDNA system (ClonceA). This CDNA was used as tester in Suppression Substractive Hybridization (SSH). The SSH-CDNA fragments were generated using the SSH-adaptor sequences ctaategectcactaraggctcgggcaggggaggtc
   AJ547930 ATAPHEU Medicago truncatula cDNA clone mtaehac110006d09, mRNA sequence.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
  1 (bases 1 to 429)
Nyamsuren,O., Colditz,F., Rosendahl,S., Bekel,T., Meyer,F., Kuester,H., Franken,P. and Krajinski,F.
First insights into the pathogenic interaction formed between the comycete Aphanomics enteiches and legumes using the model plant Medicago truncatula
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  TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 120
                         121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
CTGTTTCTTCAAATGAACAGCCTGAGAGCTGACGGCTGTCTATTACTGTGCGAGC 300
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  Contact: Krajinski F
LG Molekulargenetik
Herrenhaeuser Str. 2 D-30419 Hannover, Germany.
Location/Qualifiers
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80.1%; Pred. No. 1.7e-47;
iive 0; Mismatches 63;
   88 t
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Medicago truncatula
   ρ
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   AJ547930.1 GI:28611644
  (InVitrogen).
109 c
   Conservative
   Local Similarity
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  Unpublished
  Medicago.
  AJ547930
   EST
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  90
  61
   Query Match
   VERSION
KEYWORDS
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ORIGIN
  DEFINITION
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Site_2: EcoR1; cDNA made by oligo-dT priming.
Site_1: Rowing the following 5' adaptor: GGCACGAG(G). Size-selected >500bp
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NH MGC Library."
  BG340670 648 bp mRNA linear EST 27-FEB-2001 602462250F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4574941 5',
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   TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGAATTCCAAGAACACG 315
                                 426 GCTATTTTGACTGGTAGCCTTGACTGCTGGGGGCCCAGGGACCCTGGTCACCGTCTCCTCA 485
       298 ---AGCTIGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 354
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   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 648)
   Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Lind Mong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
found through the I.M.A.G.E. consortium/LLNL at:
http://image.llnl.gov
found through the I.M.A.G.E.
LCML285 row: d column: 14
High quality sequence stop: 648.
  1 GAGGTGCAGCTGGTGGAGTCTGGGGGGGGCTTGGCAAAGCCTGGGGGGGTCCCTGAGACTC
  THI-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
  Gaps
  10;
  Length 648;
  56; Indels
   DB 10;
   Score 224.4; DB 10
Pred. No. 9.7e-48;
0; Mismatches 56
  Contact: Robert Strausberg, Ph.D.
  BG340670.1 GI:13147108
   Query Match
Best Local Similarity 81.4%;
Matches 288; Conservative
  Homo sapiens (human)
Homo sapiens
   . .648
  mRNA sequence.
  BG340670
  148
  142
   121
  196
  181
   BASE COUNT
ORIGIN
   LOCUS
   ACCESSION
VERSION
KEYWORDS
SOURCE
   ORGANISM
   AUTHORS
TITLE
JOURNAL
   RESULT 11
BG340670
  REFERENCE
  FEATURES
   COMMENT
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BQ711467
AGENCOURT 8484867 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6300988
5', mRNA sequence.
BQ711467.1 GI:21850366
   /note="Organ: spleen; Vector: poTB7; Site_1: XhoI; Site_2: EcoR1; OndA made by oligo-dr priming. Directionally cloned into EcoR1/XhoI sites using the following 5 adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and superscript II RT (Life Technologies). Note: this is a
  110 gadgriecaderidarereraddadderiridaracaeeridaddadeereadaacere 169
   TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 120
                   CAGGCTCCAGGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
   241 CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGA-- 298
   299 ----GCTTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 354
  TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACG 354
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 920)
NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
   Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM2516 row: c column: 05
High quality sequence stop: 587.
Location/Qualifiers
                                    TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACA
   1 GAGGTGCAGCTGGAGTCTGGGGGCGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
   62.7%; Score 222; DB 13; Length 920;
80.1%; Pred. No. 4.7e-47;
ive 0; Mismatches 55; Indels 1
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/clone="IMAGE:6300989"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
   194 t
   Contact: Robert Strausberg, Ph.D.
  /organism="Homo sapiens"
   252 g
   NIH MGC Library.
-286 c 252
  Homo sapiens (human)
Homo sapiens
   Query Match
Best Local Similarity 80.1;
Matches 293; Conservative
  355
                     121
   181
  295
   source
   ORGANISM
  DEFINITION
   BASE COUNT
ORIGIN
   AUTHORS
TITLE
JOURNAL
  RESULT 14
BQ711467
LOCUS
   ACCESSION
   VERSION
KEYWORDS
SOURCE
   REFERENCE
   FEATURES
   COMMENT
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  920 bp mRNA linear EST 16-JUL-2002
.7976428 NIH_MGC_113 Homo sapiens CDNA clone IMAGE:6214426
  TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAAACGCCAACAACACA 240
   CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
   61 TGGTGCGCAGCCTCCGGGTTCAGGTTCAACTACTAACTACTACATGGACTGGGGTCCGC 120
   234
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 920)
NIH-WGC http://mgc.nci.nih.gov/.
  9
  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nth.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2381 row: 1 column: 11
High quality sequence stop: 649.
1 GAGGTGCAGCTGGTGGAGTCTGGGGGGGCGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
   þe
   12;
  Score 223.2; DB 13; Length 920;
Pred. No. 2.3e-47;
0; Mismatches 58; Indels 12;
   301 TTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCG 346
   NIH MGC Library."
272 c 259 g
  BQ708458.1 GI:21847357
  63.1%;
80.6%;
   Homo sapiens (human)
Homo sapiens
   AGENCOURT 7976428 N
5', mRNA Bequence.
BQ708458
   Matches 290; Conservative
  Similarity
   Unpublished
                         204
  181
   264
  241
  Query Match
Best Local
  VERSION
KEYWORDS
SOURCE
ORGANISM
  BASE COUNT
ORIGIN
   DEFINITION
  REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
  BQ708458
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223 CAGGCTCCAGGGAAGGGGCTGGAGGGGTTTCATACATTAGTAGTAGTGGTAGTACCATA 282
  241 CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
   283 TACTACGCAGACTCTGTGAAGGGCCGATTCACCATCTCCCAGAGAGAACACGCCAAGAACTCA
   109 GAGGTGCAGCTGGTGGAGTCTGGGGGGAGGCTTGGTACAGCCTGGGGGGGTCCCTGAGACTC
   169 recrerecedecercre----carredecricaeragrangearidaacregecee
  121 CAGGCTCCAGGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA
   TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGACGCCAACAACACA
   TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC
  completed: December 29, 2003, 21:44:18
le : 1535.8 secs
   301 TIGACTACAGGGTCTGACTCCT 322
  403 CATATAGCAGCAGCTGACGACT
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  181
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   Constructed from size fractionated cytoplasmIc mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Monaldo, Ph.D. and M. Bento Soares, Ph.D. 10.10 to 139 g 110 to 10.00 
   AW403059 456 bp mRNA linear EST 16-FEB-2000
UI-HF-BKO-aai-f-10-0-UI.rl NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3054090 5', mRNA sequence.
  284 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACAG 343
180
   CTGTTTCTTCAAATGAACAGCCTGAGAGGTGAGGACACGGCTGTCTATTACTGTGCGA-- 298
  CTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTTCTGTGCGAAA 403
   ------GCTTGACTACAGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACGTC 348
   463
   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/db_xref="taxon:9606"
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/clone="IMAGE:3054090"
/tisnue_type="lymph"
/cell_type="germinal center B cells"
/cell_type="germinal center B cells"
/cell_tine="MGC95"
/cell_the="MGC95"
/clone_lib="MHH MGC 36"
/note="Vector: pT7T3-Pac; Site_1: Not1; Site_2: Eco RI;
   Email: cgapbs-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Staudt, M.D., Ph.D.

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward.
  CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTAGTGGTGATCCCACA
  1 (bases 1 to 456)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
   Gaps
  9
  Score 221.6; DB 9; Length 456;
Pred. No. 4.5e-47;
0; Mismatches 49; Indels 6.
   Contact: Robert Strausberg, Ph.D.
   organism="Homo sapiens"
   Location/Qualifiers
  139 g
  AW403059.1 GI:6921885
  62.6%;
82.9%;
  Homo sapiens (human)
   Query Match 62.6
Best Local Similarity 82.9
Matches 267; Conservative
  . .456
   TCCTCA 354
   TCCTCA 469
  Homo sapiens
   103
   224
   181
  241
   344
   349
  464
  121
   299
   VERSION
KEYWORDS
SOURCE
ORGANISM
  source
   BASE COUNT
ORIGIN
  DEFINITION
  RESULT 15
AW403059
  AUTHORS
TITLE
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DNA encoding antiDig3 antibody heav
DNA encoding monoc
DNA encoding antiInternalising antiS. pneumoniae PPSDNA encoding antiHuman antibody hea
DNA encoding immun
DNA encoding immun
PNA encoding antiFibronectin isofor
Anti-human CTLA-4

VEGF binding relat Human KDR (VEGFR-2 Human KDR (VEGFR-2 VEGF binding relat

Human KDR

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VEGF binding relat DNA sequence for a

Anti-Bacillus anth CEA-specific antib CEA-specific antib DNA encoding anti-

Human liver single Human genome-deriv

CEA-specific antib Anti-IL-18 antibod

Chimeric antibody

Human immunoglobul

Anti-murine CTLA-4 TRO005 heavy chain DNA encoding anti-Anti-TRAIL-R antib

Human cDNA encodin

```
Anti-human CD23 5E8 moclonal antibody heavy chain variable region DNA
   Anti-human CD23 5E8 monoclonal antibody; heavy chain variable region; human CD23; IGE; FceRii/CD23; gamma-1 constant region; gamma-3 constant region; allergy; inflammation; autoimmune disease; allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss.
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148..168
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  AAL43586
ABK86789
AAS03513
AAZ55614
   AAS03461
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ABA92717
AAZ28996
   AAQ78986
   Location/Qualifiers
   AAV33310 standard; DNA; 411 BP.
   /note= "CDS
   (first entry)
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  1..57
/*tag=
  (updated)
   Macaca fascicularis
  misc_feature
   25-MAR-2003
  mat_peptide
   18-NOV-1998
  sig_peptide
  220.8
220.6
   219.4
219.4
219.2
219.2
219.2
   AAV33310;
   RESULT 1
  Antibody screening
DNA sequence for a
Antibody screening
DNA encoding a sin
   Anti-human CD23 5E
  Traget plasmid Man
  Human coding seque
   December 29, 2003, 16:08:50 ; Search time 154.453 Seconds (without alignments) 6187.013 Million cell updates/sec
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  | SIDSI/goddata/geneseq/geneseqn.embl/NA1981.DAT:
| SIDSI/goddata/geneseq/geneseqn.embl/NA1981.DAT:
| SIDSI/goddata/geneseqn.embl/NA1981.DAT:
| SIDSI/goddata/geneseqn.embl/NA1981.DAT:
| SIDSI/goddata/geneseqn.embl/NA1984.DAT:
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| SIDSI/goddata/geneseqn.embl/NA1980.DAT:
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| SIDSI/goddata/geneseq/geneseqn-embl/NA1991.DAT:
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  Description
  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*
   354
1 GAGGTGCAGCTGGTGGAGTC......TCCTGGTCACCGTCTCCTCA
  Geneseq 19Jun03:*
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.
                        GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
  Total number of hits satisfying chosen parameters:
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  Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
   US-09-019-441-4_COPY_58_411
  nucleic search, using sw model
   AAV33310
AAV61794
AAH41153
  AAL39119
ABK99213
  AAL39104
AAX36070
ABZ76706
   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
  ü
  Minimum DB seq length: 0
Maximum DB seq length: 200000000
   119
224
220
254
250
   Length DB
  19035
458
348
364
364
720
  Copyright
   Query
Match ]
   100.0
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349.2 250.4 244

Score

Result No.

Post-processing:

Database

Scoring table:

Perfect score:

6

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Sequence:

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Chimeric
Chimeric
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   misc
                AAV61794
  ö
   300
  The present sequence represents a DNA sequence encoding the heavy chain variable region of primate monoclonal antibody anti-human CD23 5E8. The invention provides primate monoclonal antibody anti-human CD23 5E8 bind human CD23, the low affinity receptor for IgE (FCeRii/CD23), and comprise either of a human gamma-1 or human gamma-3 constant region that binds to human Fc gamma receptors and inhibits IgE expression. The monoclonal antibodies of the invention are claimed to be useful for inhibiting induced IgE production for treating or preventing for inhibiting and autoimmune conditions e.g. allergic rhinitis conjunctivitis, autoimmune hameolytic anaemia, etc.
   TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 120
  177
   CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
   TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACA 240
  297
   357
  GAGGTGCAGCTGGTGGAGTCTGGGGGGGGTTGGCAAAGCCTGGGGGGTCCCTGAGACTC 117
   TGGTGCGCAGCCTCCGGGTTCACCTTCAATAACTACTACATAGACTGGGTCCGC
   GAGGTGCAGCTGGAGTCTGGGGGCGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
  CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA
   TGGTACGCAGACTCCGTGAAGGCCAGATTCACCATCTCCAGAGAGAACGCCAACAACACA
  CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGAGACACGGCTGTCTATTACTGTGCGAGC
   crerrrcravaridaacadccrdadaccidadacaccaccideccrdrcrarracrdrdcdadc
  Gaps
   354
  New anti-human CD23 monoclonal antibody - used for inhibiting IgE expression to treat or prevent allergic, inflammatory and
   TTGACTACAGGGTCTGACTCCTGGGCCAGGGAGTCCTGGTCACCGTCTCCTACA
   TTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA
  ;
0
  100.0%; Score 354; DB 19; Length 411; 100.0%; Pred. No. 3e-90; ive 0; Mismatches 0; Indels 0;
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              /*tag= e
/note= "encodes CDR 2 region"
358..378
/note= "encodes CDR 2 region"
   Example 1; Pages 108-110; 146pp; English.
  Reff ME;
   98WO-US02253
  97US-0803085.
  Kloetzer WS, Nakamura T,
   Matches 354; Conservative
 211..261
   PHARM CORP.
  auto:immune conditions
  (SEGK ) SEIKAGAKU CORP
   WPI; 1998-467495/40.
   Query Match
Best Local Similarity
  P-PSDB; AAW70380
   IDEC-) IDEC
misc_feature
   misc_feature
  05-FEB-1998;
  WO9837099-A1
   17-FEB-1998;
   20-FEB-1997;
  27-AUG-1998
  28
   61
  118
   121
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   181
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   301
   241
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"this base represents a nucleotide missing
from the sequence given in the
specification. It is included to
mainteni the nucleotide numbering in the
specification for this sequence"
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  missing
   missing
  missing
  missing
  missing
   the
  Mandy; target plasmid; gene integration; gene amplification; homologous recombination; vector; neomycin phosphotransferase; neo gene; selectable marker; immunoglobulin; CD23; 5E8; human;
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  "this base represents a nucleotide from the sequence given in the specification. It is included to maintain the nucleotide numbering specification for this sequence"
   "this base represents a nucleotide from the sequence given in the specification. It is included to maintent the nucleotide numbering specification for this sequence"
   "this base represents a nucleotide from the sequence given in the specification. It is included to maintain the nucleotide numbering specification for this sequence"
  "this base represents a nucleotide
from the sequence given in the
specification. It is included to
maintent the nucleotide numbering
specification for this sequence"
   "these bases represent nucleotides from the sequence given in the specification. They are included maintain the nucleotide numbering specification for this sequence"
   This base represents a nucleotide from the sequence given in the specification. It is included to maintain the nucleotide numbering specification for this sequence"
   Traget plasmid Mandy containing anti-CD23 gene.
   Rhesus macaque polyoma virus.
  Location/Qualifiers
   Photinus sp.
Salmonella typhimurium.
AAV61794 standard; DNA; 19035 BP.
  Mus sp.
Escherichia coli.
   - Cytomegalovirus
  Homo sapiens
  /*tag=
/note=
  721
/*tag=
/note=
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/note=
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/*tag=
  /*tag=
/note=
  - Baculovirus.
  /note=
   /note=
  /*tag=
   /note=
  2941
  3301
   feature
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  misc feature
  misc_feature
   misc_feature
  misc_feature
  misc_feature
   07-JUN-1999
  A THE SELECT OF SECOND
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| יייד פר דכמרמים              |                              | •                                                                                                                                                                       |                             |
|------------------------------|------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------|
|                              | / rcag=<br>/note=            | ent nucle                                                                                                                                                               | missing                     |
|                              |                              | from the sequence given in the<br>specification. They are included<br>maintain the nucleotide numbering<br>specification for this sequence.                             | to<br>in the                |
| misc_feature                 | 12061 /*tag=<br>/note=       | ts a<br>giver<br>is :                                                                                                                                                   | missing<br>in the           |
| misc_feature                 | 12421<br>/*tag=<br>/note=    | specification for this sequence"  "these bases represent nucleotides from the sequence given in the specification. They are included maintain the nucleotide numbering  | missing<br>to               |
| misc_feature                 | 13381<br>/*tag=<br>/note=    | specification for this sequence" k "this base represents a nucleotide from the sequence given in the specification. It is included to maintain the nucleotide numbering | missing                     |
| misc_feature                 | 14641<br>/*tag=<br>/note=    | specification for this sequence  14642                                                                                                                                  | missing<br>I to             |
| misc_feature                 | 15001<br>/*tag=<br>/note=    | sent agiven                                                                                                                                                             | missing<br>to               |
| misc_feature                 | 15961.<br>/*tag=<br>/note=   | CCHO                                                                                                                                                                    | missing<br>to               |
| misc_feature                 | 16321<br>/*tag=<br>/note=    | sent r<br>giver<br>ney ar<br>sotide                                                                                                                                     | missing<br>  to<br>  in the |
| WO9841645-A1.                |                              |                                                                                                                                                                         |                             |
| 24-SEF-1998.<br>09-MAR-1998; | 98WO-US0393                  | 3935.                                                                                                                                                                   |                             |
| 13-FEB-1998;<br>14-MAR-1997; | 98US-0023715<br>97US-0819866 | 3715.<br>9866.                                                                                                                                                          |                             |
| (IDEC-) IDEC                 | PHARM CORP.                  |                                                                                                                                                                         |                             |
| Barnett RS,                  | McLachlan                    | KR, Reff ME;                                                                                                                                                            |                             |
| WPI; 1998-521                | -521229/44.                  |                                                                                                                                                                         |                             |
|                              |                              |                                                                                                                                                                         |                             |

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9489 chécréchéchéchéandrothagachachachanachtagachachanachta 9548
  This is the nuclectide sequence of novel target plasmid Mandy.

The plasmid includes an inactivated murine dihydrofolate reductase

The plasmid includes an inactivated murine dihydrofolate reductase

ChERN gene, the Escherichia coli beta-galactosidase gene,

baculovirus DNA, a cassette comprising the promoter and enhancer

elements from cytomegalovirus and SV40 virus, the E. coli

Deta-glucuronidase (GIS) gene, firefly luciferase gene, an

inactivated Salmonella typhimurium histidinol dehydrogenase (HiSD)

gene and transposon Th5 neomycin phosphotransferase (neo) gene

sequences, in a pBR-derived backbone, and also an anti-human CD23

Igs receptor human gamma-1 monoclonal antibody 5E8 gene. The

invention provides a novel method for integrating a desired

coll vit a homologous recombination. This involves transfecting the

coll vit a homologous recombination. This involves transfecting the

coll vit a homologous recombination such as Desmond (see AAV61792), which

contains a unique sequence that is foreign to the mammalian cell

contains a unique sequence that is foreign to the mammalian cell

contains a unique sequence that is foreign to the mammalian.

followed by transfection with a 'target plasmid, such as Mandy

or Molly (see AAV61793), contraining a sequence which provides for

homologous recombination with the unique sequence on tangent of

the marker plasmid, and further comprising a desired DNA that is

to be integrated into the mammalian cells, typically an

the marker plasmid, and further comprising a desired DNA that is

to be integrated into the mammalian cells, typically an

coll and propous recombination system utilises the neo gene as a

dominant selectable marker. The neo gene is split into 3 exons.

Exon 3 is present on the marker plasmid and becomes integrated

contains a present on the marker plasmid and becomes integrated

contains and are separated by an intron into which at

the the targeting plasmid, and are separated by an intron into with the mammalian propour recombination of the targ
  TEGTECCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC
   121 CAGGCTCCAGGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA
  TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACA
  1 GAGGIGCAGCIGGIGGAGICTGGGGGCGCTTGGCAAAGCCTGGGGGGGTCCCTGAGACTC
   0; Gaps
  mammalian cells, and can be used to express any type of recombinant protein. The use of a triply spliced selectable marker means that all selected colonies arise from homologous recombination. In
  is targeted to this site, the gene is further enhanced by gene
   addition, the number of colonies that need to be screened to identify high producer clones is reduced. An amplifiable gene cabe inserted on integration of the marking vector, so that when a
   DB 19; Length 19035;
  Sequence 19035 BP; 4705 A; 4968 C; 4822 G; 4519 T; 21 other;
immunoglobulins - comprises homologous recombination using selectable marker and target plasmids.
   3; Indels
   identify high producer clones is reduced. An amp
be inserted on integration of the marking vector,
   Score 349.2; DB Pred. No. 2e-88; 0; Mismatches
  Example 1; Fig 10; 114pp; English.
   Query Match 98.6%;
Best Local Similarity 99.2%;
Matches 351; Conservative
  amplification.
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180

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301 TTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 354

CTGTTTCTTCAAATGAACAGCCTGAGGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300

241

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121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTAGTGGTGATCCCACA 180
CIGITICITICAAAIGAACAGCCIGAGAGCIGAGGACACGGCIGICIATIACIGIGCGAGC 300
                          292 CTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGA 351
   The invention relates to a novel method for screening an antibody, comprising performing 2-D electrophoresis on plural proteins in a sample. Individual protein spots are separated by reacting them with an antibody library and then replicating the bound antibodies before reacting them with the spot proteins again. The method is useful for screening an antibody specific for a target protein, e.g. from a phage antibody complementary deoxyribonucleic acid (cDNA) expression libraries as well as gene functions, and in other biological and medical sciences. This polynucleotide is a DNA sequence relating to the antibody screening
  Screening antibody; 2-D electrophoresis; plural protein; protein spot; antibody library; proteomics; ds.
  Screening an antibody using 2-D electrophoresis on plural proteins in samples for separating individual protein spots to react with an antibody library useful in proteomics and other biological sciences -
   GAGGTGCAGCTGGTGGAGTCTGGGGGCGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
   1 eacerecaecrerresaercresesaasecrresraecresesesesercereasaere
  TGGTGCGCAGCCTCCGGGTTCAGCTTCAATAACTACTACATGGACTGGGTCCGC
   rccrerecaccercre----carreaccirrascaccirarscreareacressing
  GGGTACTGGGGGTTTGACTACTGGGGCCAGGGAACCCTGGTCACGTCTCCTCA 405
  301 TIGACTACAGGGICTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 354
  Score 244, DB 24; Length 348;
Pred. No. 3.3e-59;
0; Mismatches 57; Indels (
   Sequence 348 BP; 71 A; 84 C; 108 G; 73 T; 12 other;
  Antibody screening method related DNA VH(DP-47)
   JAPAN SCI & TECHNOLOGY CORP.
JAPAN NAT CENT NEUROLOGY & PSYCHIATRY.
   Disclosure, Fig 1, 78pp, Japanese
   BP
   68.9%;
larity 82.0%;
Conservative (
   24-NOV-2000; 2000JP-0358539.
   standard; DNA; 348
   05-JUN-2001; 2001WO-JP04732
  (first entry)
   method of the invention
  WPI; 2002-471742/50.
  Query Match
Best Local Similarity
Matches 287; Conserv
   P-PSDB; AAO21548
   WO200242774-A1
   Unidentified
  02-SEP-2002
   30-MAY-2002
  χ.
    241
   352
   AAL39119
  61
  AAL39119;
   (NISC-)
  (NINA-)
  Kaneko
   AAL39119
   RESULT
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  The present invention relates to novel human monoclonal antibodies. The antibodies can bind to human Tumour Growth Factor-beta (TGF-beta) II receptor, resulting in the inhibition of the signal transduction of human TGF-beta into cells. The antibodies can be used for the prevention and treatment of diseases associated with the production of TGF-beta, such as tissue fibrosis in the lung, liver, skin, kidney or other tissues, atherosclerosis, atopy, keloid and arthritis. The present sequence was
   ij
   120
   GAGGIGCAGCIGGIGGAGICIGGGGGGGGCCIGGICAAGCCIGGGGGGICCCIGAGACTC 117
   recreteceaccircre----carreactricacracerrageareactreserics 171
   CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
  231
  TACTACACAGACTCAGTGAAGGGCCGATTCACCATCTCCAGAGACAACACCCAAGAACTCA 291
   9
   Human; antiarthritic; cardiant; monoclonal antibody; keloid; arthritis; Tumour Growth Factor-beta II receptor; TGF-beta II receptor; atopy; signal transduction inhibition; tissue fibrosis; atherosclerosis; ds.
   TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC
  cadecrecadedeaadedecrecaderecerentearecarraciadragragradara
   GAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
   Gaps
9789 TIGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 9842
  onoclonal antibodies recognizing human TGF-beta II receptor, for treating TGF-beta associated diseases such as tissue
   70.7%; Score 250.4; DB 22; Length 458; ilarity 83.9%; Pred. No. 5.6e-61; Conservative 0; Mismatches 51; Indels 6:
  Sequence 458 BP; 92 A; 121 C; 139 G; 106 T; 0 other;
   Example 12; Page 94-95; 118pp; Japanese.
  sequence SEQ ID 3.
  used in the present invention.
   17-NOV-2000; 2000WO-JP08129
   18-NOV-1999; 99JP-0328681.
08-NOV-2000; 2000JP-0340216.
   AAH41153 standard; DNA; 458
   (first entry)
   (NISB ) JAPAN TOBACCO INC.
  Kamada M;
  WPI; 2001-343825/36.
  Local Similarity
  Human monoclonal
  P-PSDB; AAB99111
   WO200136642-A1
  coding
  Homo sapiens
   18-NOV-1999;
  Sakamoto S,
   22-AUG-2001
   25-MAY-2001
  297;
  useful fo
   н
   28
   118
  172
  181
   AAH41153;
   61
  Query Match
  121
  Matches
   RESULT 3
AAH41153
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120 114

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Gaps

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181 TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAAGGCCAACAACACA 240
  TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCAGAGACAATTCCAAGAACACG 242
  CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGACACGGCTGTCTATTACTGTGCGAGC 300
   rccrerecaecererg-----garreacerrrageagerargecareagerege 122
  caescriccaeseaaesescriesaeresercricaecrarraerestresresresraeaea
   Screening antibody; 2-D electrophoresis; plural protein; protein spot;
  CAGGCTCCAGGGCAGGGCTGGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA
  NNNNNNNNNNNTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC 352
   TTGACTACAGGGTCTGACTCCTGGGGGCCAGGGAGTCCTGGTCACCGTCTC
   Antibody screening method related DNA SEQ ID No 164
   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
(NINA-) JAPAN NAT CENT NEUROLOGY & PSYCHIATRY.
   antibody library; proteomics; ds.
   05-JUN-2001; 2001WO-JP04732.
   24-NOV-2000; 2000JP-0358539.
   AAL39104 standard; DNA; 364
   (first entry)
WO200242774-A1
   Unidentified
   02-SEP-2002
  30-MAY-2002.
  ĸ
   AAL39104;
                69
   121
   123
   183
   241
   243
  301
  Kaneko
  RESULT
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  The invention relates to screening an antibody against a specific protein in an objective structure sample containing a protein group in high efficiency, comprising reacting an objective structure sample containing a protein group or a portion containing an objective protein in the sample with an antibody library, recovering the antibody combined with the protein, replicating the recovered antibody and reacting it with the objective protein at least once. The method is used for the identification of an objective protein. The present sequence is a DNA sequence for an antibody chain (derived from the DP47 heavy chain, the DPK22 light chain or a combination of the two) used in the method of
 TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGACGCCAACAACACAA 240
   CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGAACACGGCTGTCTATTACTGTGCGAGC 300
  175 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACG 234
   cremaricrecaandaacaeccidaeaeceeaeeacaeeeceeranariacrereceaaa 294
  Gaps
  Screening of an antibody used for the identification of an objective protein in high efficiency
  ;
   301 TTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTC 350
  295 NNNNNNNNNNNNTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC 344
   Score 244; DB 24; Length 364;
Pred. No. 3.4e-59;
0; Mismatches 57; Indels
  DNA sequence for antibody DP47 heavy chain variable region.
  Sequence arrayed library; SAL; ss; antibody library; protein identification; DP47; DPK22.
   Seguence 364 BP; 73 A; 90 C; 114 G; 75 T; 12 other;
  KAGAKU GIJUTSU SHINKO JIGYODAN.
KOKURITSU SEISHIN SHINKEI CENT SOCHO.
  Example 8; Page 38; 43pp; Japanese.
   ВР
   tch 68.9%; sal Similarity 82.0%; 287; Conservative (
   ABK99213 standard; DNA; 364
  07-DEC-2000; 2000JP-0373259.
  07-DEC-2000; 2000JP-0373259
  (first entry)
   WPI; 2002-579732/62.
P-PSDB; ABG69320.
   JP2002174635-A.
  invention
  Homo sapiens
  21-OCT-2002
  21-JUN-2002.
                  115
   235
  ABK99213;
   241
   Query Match
Best Local
   181
  (KAGA-)
   (KOKU-)
   Matches
   the
```

```
1;
  The invention relates to a novel method for screening an antibody, comprising performing 2-D electrophoresis on plural proteins in a sample. Individual proteins specification are separated by reacting them with an antibody library and then replicating the bound antibodies before reacting them with the spot proteins again. The method is useful for screening an antibody specific for a target protein, e.g. from a phage antibody library, which is useful in proteomics for studying various protein and complementary decoxyribonucleic acid (cDNA) expression libraries as well as gene functions, and in other biological and medical sciences. This polymucleotide is a DNA sequence relating to the antibody screening
   Screening an antibody using 2-D electrophoresis on plural proteins in samples for separating individual protein spots to react with an antibody library useful in proteomics and other biological sciences -
   Gaps
   9
   Score 244, DB 24, Length 364;
Pred. No. 3.4e-59;
0, Mismatches 57; Indels 6
   Sequence 364 BP; 73 A; 90 C; 114 G; 75 T; 12 other;
  Example 8; Page 73; 78pp; Japanese.
  Query Match 68.9%;
Best Local Similarity 82.0%;
Matches 287; Conservative (
  method of the invention.
WPI; 2002-471742/50.
```

61 TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 120

GAGGTGCAGCTGTTGGAGTCTGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 68 GAGGTGCAGCTGGTGGAGTCTGGGGGGGCGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC

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ВЪ
  67.8%;
  28-JUN-2002; 2002WO-GB03014.
  ABZ76706 standard; DNA; 720
  28-JUN-2001; 2001GB-0015841.
  (MEDI-) MEDICAL RES COUNCIL.
  (first entry)
   Conservative
   Best Local Similarity
Matches 289; Conserv
   Homo sapiens
Synthetic.
  01-MAY-2003
  09-JAN-2003
  175
   61
  121
  181
  241
   295
   ABZ76706;
   Query Match
  Key
  RESULT 8
  ABZ76706
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   The specification describes a method for screening for functional polypeptides which bind a ligand. The method comprises contacting a repertoir of polypeptides with a generic ligand, and then screening selected functional polypeptides with a target ligand. The method permits the removal from a chosen repertoire of polypeptides, those which are non-functional, e.g. as a result of the introduction of frame-shift mutations, stop codons, folding mutants or expression mutants which would be or are incapable of binding to any target ligand. The method also permits the enrichment of a chosen repertoire of polypeptides for those polypeptides which are functional, well folded and highly expressed. The polypeptides obtained can be used in
  regrececyccycceerrcagerroaccrrcaaraacracaregaegegege 120
   CAGGCTCCAGGGCAGGGGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
   TEGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACA 240
  CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGAGACACGGCTGTCTATTACTGTGCGAGC 300
   243 CTGTATCTGCAAATGAACAGCCTGAGAGGGGGGGGCGGCGGTATATTACTGGGAA 302
   rccrercrececerere----earreacerrrageacerareceareacteseres
   cadecrecadedaadedecredaderedereredecrarradregradregradada 182
   68
                                 GAGGIGCAGCIGGIGGAGICIGGGGGGGGGCTIGGCAAAGCCTGGGGGGGTCCCTGAGACIC
   303 NNNNNNNNNNNNNNNTTGACTACTGGGGCCAGGGACCCTGGTCACCGTCTC 352
  TTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTC 350
   Screening; functional polypeptide; ligand; non-functional; enrichment; single chain antibody; ScFv; 88.
  Screening for functional polypeptides which bind a ligand
  DNA encoding a single chain antibody (ScFv)
  Disclosure; Fig 2; 67pp; English.
  BP
  AAX36070 standard; DNA; 720
   98WO-GB03135
   97US-0066729
   97GB-0022131.
97US-0065428.
  (MEDI-) MEDICAL RES COUNCIL
  (first entry)
  Tomlinson I, Winter G;
  WPI; 1999-288302/24.
P-PSDB; AAY02472.
  WO9920749-A1
   20-OCT-1998;
   21-NOV-1997;
   20-OCT-1997;
  Unidentified
  15-JUL-1999
   29-APR-1999
   183
  61
  AAX36070;
  σ
  69
  123
  181
   301
  121
   241
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AAX36070

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Ä
   114
   120
  180
  CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
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diagnostic, prophylactic and therapeutic procedures. The present sequence encodes the single chain antibody (ScFv) that forms the basis of a library according to the invention.
  61 recretecacecrere----carreacerrrageacerareceargacerece
   TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC
  CAGGCTCCAGGGCAGGGGTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA
   1 GAGGTGCAGCTGGAGTCTGGGGGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
  Gaps
  Ligand; human serum albumin; HSA; antibody; cytostatic; anti-HIV; antiinflammatory; antianaemic; immunosuppressive; neuroprotective; dual-specific ligand; cancer; HIV infection; hepatitis; rubella; anaemia; inflammation; autoimmune disorder; multiple sclerosis; Crohn's disease; myasthenia gravis; gene; ds.
   344
   ;
9
   301 TTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTC 350
  /product= "HSA antibody amino acid sequence"
/note= "no start or stop codons given"
   Score 240; DB 20; Length 720;
Pred. No. 5.5e-58;
0; Mismatches 55; Indels
   Sequence 720 BP; 168 A; 181 C; 214 G; 157 T; 0 other;
   Human serum albumin antibody related DNA #1
   Winter G, Ignatovich O, Tomlinson I;
   Location/Qualifiers
1..720
/*tag= a
/partial
```

Homo sapiens.

```
The present invention describes a dual-specific ligand (I) comprising:

(a) a first single immunoglobulin variable domain with a binding specificity to a first antiate antiable domain with a binding complementary immunoglobulin single variable domain with a binding activity to a second antigen or epitope. The binding domains are mutually complementary, and the first and second domains lack mutually complementary domains that share the same specificity. (I) has cytostatic, anti-HIV, antianaemic, antiinflammatory, immunosuppressive and neuroprotective activities. The dual-specific ligand is useful for treating, preventing or diagnosing clisamsations or autoimmune disorders (e.g. multiple sclerosis, Crohn's disease or myasthenia gravis). The dual-specific ligand may be used to recruit cytotoxic T-cells to a cancer cell. The dual-specific ligand is also useful for monitoring the efficacy of drugs, as well as for monitoring toxicity. The present sequence encodes a human serum albumin (HSA) related antibody sequence, which is used in an example from the
   Dual-specific ligand having immunoglobulins with binding specificity different antigens or epitopes, useful for treating, preventing or diagnosing diseases, e.g. cancer, HIV infection, inflammations, or
  Example 1; Fig 1; 84pp; English.
WPI; 2003-210246/20.
P-PSDB; ABP95997.
   myasthenia gravis
```

GAGGTGCAGCTGGTGGAGTCTGGGGGCCGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC Gaps 9 67.8%; Score 240; DB 25; Length 720; llarity 82.6%; Pred. No. 5.5e-58; Conservative 0; Mismatches 55; Indele 6 Sequence 720 BP; 168 A; 181 C; 214 G; 157 T; 0 other; al Similarity 289; Conserv Query Match Local Matches

TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACATGGACTGGGTCCGC 120 TCCTGTGCAGCCTCTG-----GATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGC 114 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180 CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTAGTAGCACA 174 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACG 234 CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300 9 1 GAGGIGCAGCIGITGGAGICTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 61 61 115 181 175 241 121 g 셤 ઠે 셤 ď ò ò ò

CTGTATICTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAA 294

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AAD46290 standard; DNA; 348 BP

(first entry) 27-DEC-2002 AAD46290;

Human KDR (VEGFR-2) Fab heavy chain (VH) DNA from D2C6 clone.

Human; tumour; vascular endothelial growth factor receptor; metastasis; epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC; breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; gene; VH; ds.

The invention relates to a method of inhibiting tumour growth which involves administering, vascular endothelial growth factor receptor (VEGFR) antagonists in combination with radiation, chemotherapeutic agent, or epidermal growth factor receptor (EGFR) antagonist. The method is useful for inhibiting tumour growth in a human, where the tumour (e.g. tumour of the breast, heart, lung, small intestine, colon, spleen, bone, kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin, bone marrow, blood, thymus, uterus, testicles, cervix or liver) over expresses VEGFR. It is also useful for inhibiting growth of colon tumour or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR. It is preferably useful for treating subjects with both solid tumours, preferably useful for treating subjects with both solid tumours. The inhibition or reduction of tumour growth includes prevention or inhibition of the progression of tumour includes the invasiveness, metastasis, recurrence and increase in size of the tumour. The present sequence is human KDR (VEGFR-2) Fab antibody heavy chain DNA. 120 61 TCCTGTGCAGCCTCTG----GATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGC 114 121 CAGGCTCCAGGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180 181 TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGGAGGCCAACAACACA 240 115 cadgerceaegeaaegegeregagreegrerearcearragragragragragracara 174 9 Inhibiting tumor growth in humans involves administering vascular endothelial growth factor receptor antagonists in combination with radiation, chemotherapeutic agents, or epidermal growth factor receptor 1 caccinecacinecidente and increased and contract and contractions of the contract and contract 1 GAGGTGCAGCTGGTGGAGTCTGGGGGGCGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC /product= "Human KDR (VEGFR-2) Fab heavy chain (VH) /note= "CDS does not include start and stop codon" 9 DB 24; Length 348; Indels Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 other; 26; Score 238.4; DB 24 Pred. No. 1.3e-57; 0; Mismatches 56 Example 9; Page 121-122; 151pp; English. Location/Qualifiers Query Match 67.3%; Best Local Similarity 82.3%; Matches 288; Conservative 04-MAR-2002; 2002WO-US06762. 02-MAR-2001; 2001US-0798689. IMCLONE SYSTEMS INC. ď protein" /partial /\*tag= ROCKWELL P. GOLDSTEIN N I. WPI; 2002-691738/74. P-PSDB; AAE28870. WO200270008-A1 antagonists -12-SEP-2002 61 (IMCL-) (COLD/) Key 셤 8 음 8 g ð

RESULT

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invention relates to screening an antibody against a specific protein
                            CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTAGTAGTAGTAGTACTTACATA 174
   CAGGCTCCAGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
  CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
  in an objective structure sample containing a protein group in high efficiency, comprising reacting an objective structure sample containing as protein group or a portion containing an objective protein in the sample with an antibody library, recovering the antibody combined with the protein, replicating the recovered antibody and reacting it with the objective protein at least once. The method is used for the identification of an objective protein. The present sequence is a DNA sequence for an antibody chain (derived from the DP47 heavy chain,
  light chain or a combination of the two) used in the method of
  GAGGTGCAGCTGGTGGAGTCTGGGGGGCGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
   TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACAC
   Screening of an antibody used for the identification of an objective protein in high efficiency
   301 TIGACTACAGGGICTGACTCCTGGGCCCAGGGAGTCCTGGTCACCGTCTC 350
  GICACAGATGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTC 344
   66.9%; Score 237; DB 24; Length 742; 80.6%; Pred. No. 3.9e-57;
  Sequence 742 BP; 152 A; 186 C; 225 G; 155 T; 24 other;
   Sequence arrayed library; SAL; ss; antibody library; protein identification; DP47; DPK22.
   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
(KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.
   0; Mismatches
  DNA sequence for antibody DP47VH/DPKS22VL.
   Example 8; Page 38; 43pp; Japanese.
  BP.
  07-DEC-2000; 2000JP-0373259
   07-DEC-2000; 2000JP-0373259.
  ABK99212 standard; DNA; 742
   (first entry)
   Query Match
Best Local Similarity 80.6
Matches 283; Conservative
  WPI; 2002-579732/62
  JP2002174635-A.
   sapiens
   21-OCT-2002
  21-JUN-2002.
   Synthetic.
   115
  241
   295
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      121
   181
   ABK99212;
  CHOH
  RESULT 11
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   a
   The invention relates to a novel antibody having a first antigen binding stee specific for a first vascular endothelial growth factor (VEGF) receptor and a second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of the VEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leukaemia cells. The antibodies are useful for treating tumours and for in vivo or in vitro for investigative and diagnostic
   TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 120
  TCCTGTGCAGCCTCTG-----GATTCACTTCAGTAGCTATAGCATGAACTGGGTCCGC 114
                                   9
  methods. This polynucleotide sequence represents a human DNA sequence relating to the bispecific antibodies that bind to the VEGF receptors of
  mitogenesis;
  1 GAGGTGCAGCTGGTGGAGTCTGGGGGGCTTGGCAAAGCCTGGGGGGGTCCCTGAGACTC
   gaegrecaecrecaecaercrecececaeccrecrescreaecresececerecereaecre
   æ
  Gaps
   New bispecific antibodies having antigen-binding sites specific for first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia
   TTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTC 350
   Grcacagargerrrrigararcriggiccaagggacaarggreacercric 344
  9
   Length 348;
  Cytostatic, antibody, antigen binding site, VEGF receptor, r
leukaemia cell; vascular endothelial growth factor; tumour;
bispecific antigen-binding protein; human; gene; ds.
  56; Indels
  Score 238.4; DB 25;
Pred. No. 1.3e-57;
0; Mismatches 56;
   Seguence.348 BP; 82 A; 85 C; 105 G; 76 T; 0 other;
  VEGF binding related DNA SEQ ID No 75.
  Disclosure; Page 70; 98pp; English
  BP.
   for treating tumors
  67.3%;
nilarity 82.3%;
Conservative 0
  ABT23325 standard; DNA; 348
  26-JUN-2002; 2002WO-US20332.
   26-JUN-2001; 2001US-301299P
   (IMCL-) IMCLONE SYSTEMS INC
   (first entry)
  WPI; 2003-201468/19.
P-PSDB; ABJ26763.
  Similarity
   WO2003002144-A1
  the invention
   Homo sapiens
   01-MAY-2003
  Local Simi
hes 288;
  09-JAN-2003
   ٦
   5
  235
   301
   295
   ABT23325;
  Query Match
  zhu Z;
  Matches
  ABT23325
ID ABT
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9 68

Gaps

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62;

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Gaps

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Indels

62;

Mismatches

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Conservative

283;

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Matches
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                           TCCTGTGTGCAGCCTCTG----GATTCACCTTTAGTAGTTATGCCATGAGCTGGGTCCGC 122
   CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
   TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGACGCCAACAACACACA
  CTGTTTCTTCAAATGAACAGCCTGAGAGCTGACACGCTGTCTATTACTGTGCGAGC 300
   The invention relates to a novel method for screening an antibody, comprising performing 2-D electrophoresis on plural proteins in a sample. Individual protein spots are separated by reacting them with an antibody library and then replicating the bound antibodies before reacting them with the spot proteins again. The method is useful for screening an antibody specific for a target protein, e.g. from a phage antibody library, which is useful in proteomics for studying various protein and complementary deoxyribonucleic acid (cDNA) expression libraries as well as gene functions, and in other biological and medical sciences. This polymucleotide is a DNA sequence relating to the antibody screening
  Screening antibody; 2-D electrophoresis; plural protein; protein spot;
   Screening an antibody using 2-D electrophoresis on plural proteins in samples for separating individual protein spots to react with an antibody library useful in proteomics and other biological sciences -
TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC
   TATTATGCAGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACTCCAAGAACACC
  NNNNNNNNNNNNTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCC 353
  TTGACTACAGGGTCTGACTCCTGGGGGCCAGGGAGTCCTGGTCACCGTCTCC 351
  Antibody screening method related DNA SEQ ID No 163
   Seguence 742 BP; 152 A; 186 C; 225 G; 155 T; 24
   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
(NINA-) JAPAN NAT CENT NEUROLOGY & PSYCHIATRY.
  Example 8; Page 72; 78pp; Japanese.
  antibody library; proteomics; ds
   AAL39103 standard; DNA; 742 BP.
   05-JUN-2001; 2001WO-JP04732
  24-NOV-2000; 2000JP-0358539
   (first entry)
   method of the invention.
  WPI; 2002-471742/50.
  WO200242774-A1
   Unidentified
  02-SEP-2002
   30-MAY-2002
                            69
   181
  241
  301
  303
  AAL39103;
   121
  123
   183
   243
   Kaneko
   RESULT 12
  AAL39103
ID AAL3
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```

66.9%; Score 237; DB 24; Length 742; 80.6%; Pred. No. 3.9e-57;

Query Match Best Local Similarity

other;

```
180
  183 TATTATGCAGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACTCCAAGAACACC 242
   CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
   120
  recrerecadecrere----carreacerragiagramaceareacerederece
   123 caagciccadegaadedecredadrecrerereratiadrecadrecredadedecada 182
  9
                           68
   Human, tumour; vascular endothelial growth factor receptor; metastasis; epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC; breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; gene;
   Inhibiting tumor growth in humans involves administering vascular endothelial growth factor receptor antagonists in combination with radiation, chemotherapeutic agents, or epidermal growth factor receptor
   CAGGCTCCAGGGCAGGGCTGGGAGTCTCACGTATTAGTAGTAGTGGTGATCCCACA
GAGGTGCAGCTGGTGGAGTCTGGGGGGCGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
                             GAGGTGCAGCTGTTGGAGTCTGGGGGGGTTTTGGTACAGCCTGGGGGGGTCCCTGAGACTC
  TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC
   /*tag= a
/product= "Human KDR (VEGFR-2) Fab heavy chain (VH)
  /note= "CDS does not include start and stop codon" 
partial
  301 TTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCC 351
  NNNNNNNNNNNTTIGACTACTGGGCCAGGGAACCCTGGTCACCGTCTCC 353
   Human KDR (VEGFR-2) Fab heavy chain (VH) DNA from D1H4 clone.
  Example 12; Page 124-125; 151pp; English.
   Location/Qualifiers
   ВР
   IMCLONE SYSTEMS INC. ROCKWELL P.
   AAD46292 standard; DNA; 348
   02-MAR-2001; 2001US-0798689
  04-MAR-2002; 2002WO-US06762
  (first entry)
  protein"
   1..348
/*tag=
  GOLDSTEIN N I.
   WPI; 2002-691738/74.
P-PSDB; AAE28870.
   WO200270008-A1
   Homo sapiens.
  27-DEC-2002
   antagonists
  12-SEP-2002
 Н
                             σ
   69
  181
  241
  243
   303
   AAD46292;
  61
   121
  (ROCK/)
  (IMCI-)
  VH; ds
  RESULT 13
   Key
   AAD46292
```

```
The invention relates to a method of inhibiting tumour growth which involves administering, vascular endothelial growth factor receptor (VEGFR) antagonists in combination with radiation, chemotherapeutic agent, or epidermal growth factor receptor (EGFR) antagonist. The method is useful for inhibiting tumour growth in a human, where the tumour (e.g. tumour of the breast, heart, lung, small intestine, colon, spleen, bone, kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin, bone marrow, blood, thymus, uterus, testicles, cervix or liver) over expresses VEGFR. It is also useful for inhibiting growth of colon tumour or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR. It is preferably useful for treating subjects with both solid tumours, preferably high vascular tumours and non-solid tumours. The inhibition or reduction of tumour growth includes prevention or inhibition of the progression of tumour including cancerous and non-cancerous tumours, where the progression of tumours includes the invasiveness, metastasis, recurrence and increase in size of the tumour. The present sequence is human KDR (VEGFR-2) Fab antibody heavy chain DNA.
```

Seguence 348 BP; 82 A; 86 C; 104 G; 76 T; 0 other;

```
TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 120
   CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
  CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
   CTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTTTACTGTGCGAGA 294
   rccrerecaecercresarrca----cerreagracerarascarsaacressress 114
  115 caggcrccagggaaggggcrgagrgggcrcrccarragragragragracran 174
   TACTACGCAGACTCAGTGAAGGCCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCA 234
   1 GAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTGGGGGGGTCCCTGAGACTC 60
  9
  GAGGICCAGCIGGICCAGICTGGGGGGGGCCTGGTCAAGCCTGGGGGGGTCCCTGAGACTC
                                     Gaps
  TIGACTACAGGGICTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTC 350
                                     9
66.9%; Score 236.8; DB 24; Length 348; 82.0%; Pred. No. 3.6e-57; indels 6;
                  Best Local Similarity 82.0
Matches 287; Conservative
  175
  235
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     Query Match
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Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis; leukaemia cell; vascular endothelial growth factor; tumour; bispecific antigen-binding protein; human; gene; ds.
  VEGF binding related DNA SEQ ID No 79
       ABT23327 standard; DNA; 348
  (first entry)
   WO2003002144-A1.
  Homo sapiens
  01-MAY-2003
                              ABT23327;
ABT2332
           #X#XBX#X8X#X#X#X#X#X#X#
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```
The invention relates to a novel antibody having a first antigen binding site specific for a first vascular endothelial growth factor (VEGF) receptor and a second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of the VEGF receptor and are useful for reducing proteins block activation of the VEGF receptor and are useful for reducing or inhibiting VEGF-induced and migration of leukaemia cells. The antibodies are useful for treating tumours and for in vivo or in vitro for investigative and diagnostic methods. This polynucleotide sequence represents a human DNA sequence relating to the bispecific antibodies that bind to the VEGF receptors of
   CTGTTTCTTCAAATGAACAGCCTGAGAGCTGACACGGCTGTCTATTACTGTGCGAGC 300
   rccrieneciaecircresarrca----cerreagrascrarascareaacreserces 114
  CAGGCTCCAGGGCAGGGCTGGAGTGGGTCTCCACGTATTAGTAGTAGTGGTGATCCCACA 180
   cadecrecadedaadedecredadredererererereriadradradradradradra 174
  CTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGA 294
   1 caccircacinericacitricacionesconocinas de la caccine de 
  TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGGAACGCCAACACACA
  TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACTACATGGACTGGGTCCGC
   TACTACGCAGACTCAGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCA
  1 GAGGTGCAGCTGGAGTCTGGGGGGCGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
   Gaps
   ø
  New bispecific antibodies having antigen-binding sites specific fo
first vascular endothelial growth factor (VEGF) receptor and for s
second VEGF receptor, useful for inhibiting migration of leukemia
   9
   301 INGACIACAGGGICTGACTCCTGGGCCCAGGGAGTCCTGGTCACCGTCTC 350
  Grcacagaricarinidararchicoccoaacagacaaricarchicorchicosta
  DB 25; Length 348;
   Indels
   Sequence 348 BP; 82 A; 86 C; 104 G; 76 T; 0 other;
  Score 236.8; DB 25;
Pred. No. 3.6e-57;
0; Mismatches 57;
  Disclosure; Page 72; 98pp; English
   cells, or for treating tumors -
  Query Match 66.9%;
Best Local Similarity 82.0%;
Matches 287; Conservative
                                  (IMCL-) IMCLONE SYSTEMS INC.
  WPI; 2003-201468/19
  the invention.
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Human; tumour; vascular endothelial growth factor receptor; metastasis; epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC; breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; gene; Human KDR (VEGFR-2) Fab heavy chain (VH) DNA from D2H2 clone. AAD46294 standard; DNA; 348 BP. 27-DEC-2002 (first entry) AAD46294; VH; da AAD46294
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AC AAD4
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HOM

Homo sapiens

26-JUN-2002; 2002WO-US20332 26-JUN-2001; 2001US-301299P.

09-JAN-2003

```
The invention relates to a method of inhibiting tumour growth which involves administering, vascular endothelial growth factor receptor (VEGFR) antagonists in combination with radiation, chemotherapeutic agent, or epidermal growth factor receptor (EGFR) antagonist. The method is useful for inhibiting tumour growth in a human, where the tumour (e.g. tumour of the breast, heart, lung, small intestine, colon, spleen, bone, kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin, bone marrow, blood, thymus, uterus, testicles, cervix or liver) over cxpresses VEGFR. It is also useful for inhibiting growth of colon tumour or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR. It is preferably useful for treating subjects with both solid tumours. The inhibition or reduction of tumour growth includes prevention or inhibition of the progression of tumour including cancerous and non-cancerous tumours, where the progression of tumours includes the invasiveness, metastasis, recurrence and increase in size of the tumour. The present sequence is human KDR (VEGFR-2) Fab antibody heavy chain DNA.
  CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
   CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
   TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGGACGCCAACAACACA 240
   rccrerecaeccrcregarrca ----ccrrcagragerarageargaacregercee 114
   casscriccasssaassescrissasressrcricarccarrastrasrasrasrasrasrana 174
  175 racracecagacreagreaaeeeccearreacearcrecagagacaaeeccaaeeacrea 234
  Inhibiting tumor growth in humans involves administering vascular endothelial growth factor receptor antagonists in combination with radiation, chemotherapeutic agents, or epidermal growth factor receptor
  1 GAGGTGCAGCTGGTGGAGTCTGGGGGGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
   GAAGTGCAGCTGCAGTCTGGGGGGGGGCTGGTCAAGCCTGGGGGGTCCCTGAGACTC
  Gaps
                                    1..348
/*tag= a
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/note= "CDS does not include start and stop codon"
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  58; Indels
  Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 other;
  Example 12; Page 126; 151pp; English
                  Location/Qualifiers
   IMCLONE SYSTEMS INC. ROCKWELL P.
   04-MAR-2002; 2002WO-US06762
   02-MAR-2001; 2001US-0798689
  Best Local Similarity 81.7
Matches 286; Conservative
  /partial
   GOLDSTEIN N I.
   WPI; 2002-691738/74.
   P-PSDB; AAE28873
  #O200270008-A1
  12-SEP-2002.
  antagonists
   61
   61
   121
   115
   181
  Query Match
  241
   (IMCL-)
(ROCK/)
(GOLD/)
                  Key
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235 CTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGA 294
  295 grcacagargerririgararcrigedeceaaggacaargercacegrere 344
   301 TIGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTC
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Sequence

Sequence

Sequence

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Run on:

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Database

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APPLICANT: RICHERF, Mitchell E.
APPLICANT: KLOETZER, Milliam S.
APPLICANT: NKLOETZER, Milliam S.
APPLICANT: NKLOETZER, MILLIAM S.
APPLICANT: NARAUTA, TAKABIA,
TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
NUMBER OF SEQUENCES: 35
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
CITY: Alexandria
STATE: Virginia
  Length 411;
   CCUNTRY: United states

Z19: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FEB-1997
CLASSIFICATION NUMBER: 19,030
FILING STEATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-620
TELEPHONE: (703) 836-6620
  DB 3;
  PCT-US93-10555-37
US-08-958-201-5
US-08-545-809A-53
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   Sequence 4, Application US/08803085
Patent No. 6011138
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  STATE: Virginia
COUNTRY: United States
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EDNESS: single
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58..411
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Sequence 21
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(c) 1993 - 2003 Compugen Ltd.
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Maximum DB seq length: 200000000
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Match Length DB
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  APPLICANT: Cirino, Nick M
APPLICANT: Cirino, Nick M
APPLICANT: Carino, Paul J
APPLICANT: Lehnert, Bruce E
TITLE OF INVENTION: Disruption of Anthrax Toxin Binding to Cell Surface
TITLE OF INVENTION: Receptors
FILE REFERENCE: S-89,662
CURRENT APPLICATION NUMBER: US/09/273,839A
CURRENT FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
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  2 AGGIGCAGCIGGAGICIGGGGGGGCCTIGGCAAAGCCTIGGGGGGTCCCTGAGACTCT
  9793 TIGACTACAGGGTCTGACTCCCTGGGGCCCAGGGAGTCCTGGTCACCGTCTCCTCA 9847
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   Query Match 62.4%; Score 220.8; DB 4; Best Local Similarity 80.1%; Pred. No. 3.3e-59; Matches 290; Conservative 0; Mismatches 57;
  US-08-652-816A-21

Sequence 21, Application US/08652816A

Patent No. S872215

GENERAL INFORMATION:

APPLICANT: Osbourn, JK
  Sequence 9, Application US/09273839A Patent No. 6329156 GENERAL INFORMATION:
   TYPE: DNA
ORGANISM: Homo sapiens
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CA 459
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  US-09-273-839A-9
   US-09-273-839A-9
  122
   242
  338
   353
        181
  SEQ ID NO 9
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  9553 TCCTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 9612
   9613 CAGGCTCCAGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTAGTGGTGATCCCACA 9672
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   9493 GAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC 9552
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  240
  300
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   117
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  CIGITICTICADANGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 357
  TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 120
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| Sequence 3, Application US/09343485A |
| Sequence 3, Application US/09343485A |
| Sequence 3, Application US/09343485A |
| Setent No. 6413777 |
| GENERAL INFORMATION: |
| APPLICANT: REFF, MITCHELL R. |
| APPLICANT: BARNETT, RICHARD S. |
| APPLICANT: BARNETT, RICHARD S. |
| TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES I TITLE OF INVENTION: MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION NOVERT OF ACCOMPLISHING THE SAME |
| TITLE OF INVENTION: WARMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION NUMBER: US/09/343,485A |
| CURRENT ELLING DATE: 1999-06-30 |
| PRIOR APPLICATION NUMBER: 09/023,715 |
| PRIOR FILLING DATE: 1997-03-14 |
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   OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: referred to as "Mandy"
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  DB 4; Length 19040;
   Query Match 95.5%; Score 338.2; DB 4; Length Best Local Similarity 98.9%; Pred. No. 3.8e-95; Matches 351; Conservative 0; Mismatches 3; Indels
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        Pred. No. 8.8e-101;
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  TYPE: DNA
ORGANISM: Artificial Sequence
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241

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121

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Gaps

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   Sequence 22, Application US/08652816A
Patent No. 5872215
GENERAL INFORMATION:
APPLICANT: OSDOUTH, JK
APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and TITLE OF INVENTION: EASONERS SJ
CORRESPONDENCE ADDRESS: SJ
CORRESPONDENCE ADDRESS: Asteball, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
   CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

FILING DATE:

PRIOR APPLICATION DATA:

FILING DATE:

APPLICATION NUMBER:

FILING DATE:

APPLICATION DATA:

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FILING DATE:

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FILING DATE:

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APPLICATION NUMBE
  FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: DAVIG W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELEBHONE: 312-474-6300
INFORMATION FOR SEQ 1D NO: 22:
  STATE: Illinois
COUNTRY: United States of America
CONDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   SEQUENCE CHARACTERISTICS:
  354 base pairs
  STREET: 6300 S
CITY: Chicago
  STRANDEDNESS
  RESULT 5
JS-08-652-816A-22
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   2 AGGTICAGCTGGTGCAGTCTGGGGGGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCT 61
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  12; Gaps
APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'TO-'
STREET: 6300
  DB 2; Length 354;
   CUTY: Chicago
STATE: Illicis Chicago
STATE: Chicago
COUNTRY: United States of America
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
RRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
RRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
RRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
RRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 920634.6
FILING DATE: CA-DEC-1995
RRIOR APPLICATION NUMBER: GB 9610824.6
FILING DATE: CA-DEC-1995
RRIOR APPLICATION NUMBER: US 08/244.597
FILING DATE: CA-DEC-1997
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Pred. No. 2.6e-59;
0; Mismatches 59; Indel8
   REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
  Query Match 62.3%;
Best Local Similarity 80.2%;
Matches 288; Conservative
  TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
   LENGTH: 354 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
   linear
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US-08-652-816A-21
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TOPOLOGY: linear
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  61 TCCTGTGCAGCCTCTG-----GATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGC 114
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   235 CTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGA 294
  300 ----CTTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 354
   295 GCTTTGGTTCGGGGAGTTATAAAGGACTGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 354
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  Sequence 48, Application US/08545809A
Sequence 48, Application US/08545809A
BEREAL NO. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matuda, Funihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
   12;
  Length 354;
   60; Indels
  1 GAGGTGCAGCTGGTGGAGTCTGGGGGGCGCTTGGCAAAGCCTGGGGGG
  Score 220; DB 2;
Pred. No. 3.9e-59;
0; Mismatches 60
   MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPPERATING SYSTEM: Windows95
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
FILING DATE: 27-MAR-1997
APPLICATION UNDERF: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
  NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFREENCE/DOCKET NUMBER: 0650
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
  62.1%;
80.0%;
   LENGTH: 743 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
  TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
   Matches 288; Conservative
  ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
      linear
  Query Match
Best Local Similarity
   Boston
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  US-08-545-809A-48
    ; TOPOLOGY:
US-08-652-816A-22
  COUNTRY:
  STATE:
   121
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393
  61 TEGTECCCAGCCTCCGGGTTCACGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 120
  394 rccricrockáccricrá----darrckácrrckárkacráradckrákartádárcca 447
   121 CAGGCTCCAGGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTAGTGATCCCACA 180
  448 CAGGCTCCAGGGAAGGGGCTGGAGTGGGTTTCATACATTAGTAGTAGTAGTAGTAGTACCATA 507
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   Length 743;
  Sequence 24, Application US/08652816A

Patent No. 587215

GENERAL INFORMATION:
APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
APPLICANT: Allen, DJ
APPLICANT: MCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEBE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
   STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: 111inois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PC Compatible
OPERATING SYSTEM: PC Compatible
OPERATING SYSTEM: PC Compatible
OPERATING SYSTEM: PC COMPATIBLE
OPERATION UNIMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
  Indels
  62.0%; Score 219.4; DB 3;
86.0%; Pred. No. 8.4e-59;
iive 0; Mismatches 36;
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
  JMBER: GB 9206318.9
24-MAR-1992
   FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
   PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
   UMBER: GB 9206372.6
23-SEP-1992
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: human lymphoblast
CELL LINE: CGM1
  Best Local Similarity 86.0
Matches 257; Conservative
   PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB
FILING DATE: 24-MAR-19
PRIOR APPLICATION NUMBER: GB
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FastSEQ for Windows Version 2.0
  29,066
FR: 06501/004001
  APPLICATION NUMBER: US/08/545,809A FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/JP93/00603 FILING DATE: 10-MAY-1993 ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
   Sequence 21, Application US/08545809A Patent No. 6096878 GENERAL INFORMATION:
  NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 065/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-8070
TELEFAX: 617-542-8906
   Homo sapiens
human lymphoblast
   INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 715 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: Genomic DNA ORIGINAL SOURCE:
   STREET: 225 Franklin Street
  Query Match 61.7%;
Best Local Similarity 85.9%;
Matches 256; Conservative (
   COMPUTER READABLE FORM MEDIUM TYPE: Disket: COMPUTER: IBM Compa
                            CURRENT APPLICATION
   ZIP: 02110-2804
  ns
   ; CELL TYPE:
; CELL LINE:
US-08-545-809A-11
   JS-08-545-809A-21
        SOFTWARE:
  ORGANISM:
  COUNTRY:
   g
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   61 TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 120
   61 TCCTGTGCAGCCTCTG-----GATTCACCTTTGATGATTATGGCATGAGCTGGGTCCGC 114
   115 CAAGCTCCAGGGAAGGGGCTGGAGTGGTCTCTGGTATTAATTGGAATGGTGGTAGCACA 174
   175 GGTTATGCAGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCC 234
   CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
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  1 GAGGTGCAGCTGGTGGAGTCTGGGGGGTGCTGGTACGGCCTGGGGGGTCCCTGAGGCTC 60
   Sequence 11, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Mateuda, Pumhinko
TITLE OF INVENTION: BEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
   301 TTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTC 350
   295 AGGCGGTATGCGTTGGATTATTGGGCCAAGGTACCCTGGTCACCGTGTC 344
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   DB 2;
PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIOR APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 01-DEC-1992
APPLICATION NUMBER: 03-04
ATTORNEY/AGENT INFORMATION:
NAME: DAVIG W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/POCKET NUMBER: 28111/33308
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 base pairs
TYPE: NUCLEIC acid
TYPE: NUCLEIC acid
   Pred. No. 6.96
0; Mismatches
  61.9%; Score 219.2; ilarity 78.9%; Pred. No. 6.9 Conservative 0; Mismatches
   E: Fish & Richardson, P.C. 225 Franklin Street
   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compati
   linear
  Query Match
Best Local Similarity
Matches 276; Conserv
   COUNTRY: US
ZIP: 02110-2804
   STREET: 225 1
CITY: Boston
   TOPOLOGY:
US-08-652-816A-24
   US-08-545-809A-11
   STATE:
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   APPLICANT: HONGO, Taguku
APPLICANT: Matguda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
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Score 218.4; DB 3;
Pred. No. 1.7e-58;
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Patent No. 5419904
GENERAL INFORMATION:
GENERAL ITIE, Reiko F
TITLE OF INVENTION: SECRETING ANTI-GANGLIOSIDE ANTIBODY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: Poms, Smith, Lande & Rose
STREET: 2029 Century Park East, Suite 3800
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
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APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 29,066
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REFERENCE/DOCKET NUMBER: 29,066
REFERENCE/SOFTSTATION:
TELECOMMUNICATION:
TELEPHONE: 617-542-8906
  United States of America
  TELEFAX: 0.1
TELEX: 200154
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 519 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
   ORGANISM: Homo sapiens
CELL TYPE: human lymphoblast
CELL LINE: CGM1
US-08-545-809A-21
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
   Query Match 61.5%;
Best Local Similarity 85.6%;
Matches 256; Conservative
  Genomic DNA
   CITY: Los Angeles
STATE: California
COUNTRY: United States
  linear
  TOPOLOGY: line
MOLECULE TYPE: C
ORIGINAL SOURCE:
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US-08-026-320A-1
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1 CCATION: 397.429

1 OCHER INFORMATION: /function= "Complementary determining

1 OTHER INFORMATION: region 3 (CDR3)"

US-08-026-320A-1
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CELL LINE: L612
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OTHER INFORMATION: /function= "Complementary
OTHER INFORMATION: determining region 2 (CDR2)"
  determining region 1 (CDR1)"
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Best Local Similarity 79.0%; Pred. No. 1e-57;
Matches 289; Conservative 0; Mismatches 59;
  /function= "Complementary
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/026,320A
FILING DATE: 26-FEB-1993
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION: 424
APPLICATION NUMBER: US 07/609803
FILING DATE: 05-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J
REGISTRATION NUMBER: 29421
REFERENCE/DOCKET NUMBER: 94268
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310771297
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPPOLGGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
HYPOTHETICAL: NO
HYPOTHETICAL: NO
HYPOTHETICAL: NO
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  Region Sequence"
  NAME/KEY: misc_feature
LOCATION: 148.162
OTHER INFORMATION: /fur
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  NAME/KEY: misc feature
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   Sequence 11, Application US/09273839A
Fatent No. 6329156
GENERAL INFORMATION:
APPLICANT: Cirino, Nick M
APPLICANT: Cachert, Bruce E
TITLE OF INVENTION: Disruption of Anthrax Toxin Binding to Cell Surface;
TITLE OF INVENTION: Receptors;
TITLE OF INVENTION: Receptors;
TITLE OF INVENTION: Receptors;
CURRENT APPLICATION NUMBER: US/09/273,839A
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CURRENT FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
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  104 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGCTCCAGCCTGGGAGGTCCCTGAGACTCT 163
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  338 TGTATCTGCAAATAAACAGTCTGAGAGACGAGGACACGGCTGTGTATTACTGTGCCAGAG 397
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  2 AGGTGCAGCTGGTGGAGTCTGGGGGGGGCTTGGCAAAGCCTGGGGGGGTCCCTGAGACTCT
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  Gaps
  GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REPERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
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US-10-039-785-65
; Sequence 65, Application US/10039785
; Patent No. 6538938
   Query Match
Best Local Similarity 79.5%;
Matches 283; Conservative
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CORGANISM: Homo sapiens
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  rccrch 417
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US-09-273-839A-11
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  242
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240
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   115 caescriccaeseaaesescriesacriesercricaecrarrasresrasresresrascaea 174
   175 TACTACGCAGACTCCGTGAAGGCCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACG 234
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   9
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Sequence 23, Application US/08545809A

Sequence 23, Application US/08545809A

Patent No. 6096818

GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku

TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: BEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 225 Franklin Street
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   DB 4;
   Score 214.6; DB 4
Pred. No. 2.6e-57;
0; Mismatches 39
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PRIOR FILING DATE: 2002-04-05
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PRIOR FILING DATE: 2001-12-20
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PRIOR FILING DATE: 2001-11-04
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PRIOR PILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-09-99
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
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Matches 254; Conservative 0
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   COUNTRY:
  121
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COMPUTER READABLE FORM
   NAME/KEY:
LOCATION:
  TOPOLOGY:
   US-08-428-197-35
   301
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   TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF TITLE OF INVENTION: WARTABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH TITLE OF INVENTION: THEREOF TITLE OF INVENTION: THEREOF NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
STORESSEE: Spension: Spension: Store Sto
  170 gaggreczácrierregagreregegegecriregracagecriegegegerecreagaere 229
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   E: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
   PALLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
RIOR APPLICATION DATE:
APPLICATION DATE:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECHONE: 617-542-5070
   06501/004001
  Sequence 35, Application US/08428197
Patent No. 5891438
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
   ORGANISM: Homo sapiens
CELL TYPE: human lymphoblast
CELL LINE: CGM1
  TELEX: 200154
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 514 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
  Query Match 60.3%;
Best Local Similarity 84.9%;
Matches 253; Conservative
  TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
  CITY: Los Angeles
STATE: California
COUNTRY: USA
   US-08-545-809A-23
  RESULT 14
US-08-428-197-35
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APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
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TITLE OF INVENTION: THEREOF
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  recearicaritricaratericides de caracidar de contra de co
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6
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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Pred. No. 1e-56;
0; Mismatches 63;
  PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: HOWells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2630
TELECOWNUNICATION INFORMATION:
TELECOWNUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5110
SEQUENCE CHARACTERISTICS:
FROMTH: 351 basis
  PCT-US93-10555-35; Sequence 35, Application PC/TUS9310555; GENERAL INFORMATION:
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   59.9%;
  LENGTH: 351 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  Query Match
Best Local Similarity 79.5
Matches 279; Conservative
  linear
  IMMEDIATE SOURCE:
CLONE: SpA3-33
  MOLECULE TYPE:
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   241 CTGCAAATGAACAGCCTGAGAGCCGAAGACACGGCTGTGTATTACTGTGCGAGAGATGCA 300
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  306 -- TACAGGGTCTGACTCCTGGGGCCAGGAGTCCTGGTCACCGTCTCA 354
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   COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER IN PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/10555

FLISG FILING DATE: 29-OCT-1993

CLASSIFICATION: Stacy L.

NAME: Howells, Stacy L.

REGISTRATION NUMBER: P7-2630

TELEPAN: (619) 455-5100

TELEPAN: (619) 455-5100

TELEPAN: (619) 455-5100

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 351 base pairs

TYPE: MICLEIC ACID
E: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
  Best Local Similarity 79.5
Matches 279; Conservative
                STREET: 1880 CITY: Los Angeles
  ADDRESSEE:
   PCT-US93-10555-35
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Search completed: December 29, 2003, 21:48:31 Job time : 39.9667 secs

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Appl Appl Appl Appl Appl Appl

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Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Database

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  Sequence 118,
  Sequence 191,
Sequence 67, 7
   Sequence 4, Application US/09019441
Publication No. US20030086921A1
GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
KLOFTZER, William S.
NAKAMURA, Takehiko
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   NUMBER OF SEQUENCES:
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FILING DATE: 05-P6-1998
CLASSIFICATION AND AND INERCOF AS I
3 US-09-969-748C-1
2 US-10-309-764-134
2 US-10-309-764-70
2 US-10-309-764-70
2 US-10-309-764-94
2 US-10-309-764-14
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   NAME: TESKIN, ROBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-502
TELECOMMUNICATION INFORMATION:
   APPLICATION NUMBER: US 08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
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TELEPHONE: (703) 836-6620 TELEFAX: (703) 836-2021 INFORMATION FOR SEQ ID NO: 4:

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Result No.

Sequence

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Patent No. US20020068276A1

GENERAL INFORMATION:
APPLICANT: Winter, Greg

APPLICANT: Winter, Greg

TITLE OF INVENTION: Methods for Selecting Functional Peptides
FILE REFERENCE: 3789/72916

CURRENT APPLICATION UMBER: US/09/192,854

CURRENT PILING DATE: 1998-11-17

EARLIER PILING DATE: 1999-11-21

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                             NATIONAL TOWNS TO THE TOWN TOWNS TO THE TERENCE TOWN NUMBER: 35,030
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TELEPHONE: (703) 836-6620
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STRANDEDNESS: single
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Matches 354; Conservative
  SOFTWARE: Patentin Ver. 2.
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Publication No. US20030059424A1
GENERAL INFORMATION: Atchell E.
KLOETZER, William S.
NAKAMURA, Takehiko
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
ANTIBODIES AND USE THEREOF AS THERAPEUTICS
   ö
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   Version #1.30
  NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSES: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
CITY: Alexandria
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100.0%; Pred. No. 4.6e-102;
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ZIE: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
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FILING DATE: 25-Mar-2002
CLASSIFICATION: <UNKNOWN>
   APPLICATION NUMBER: US/08/803,085
   SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-09-019-441-4
  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
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LENGTH: 411 base pairs
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Sequence.1, Application US/09968744A

; Sequence.1, Application Wo. US20030148372A1
; Publication No. US20030148372A1
; GENERAL INFORMATION:
    APPLICANT: Tomilinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; TILE REFERENCE: 8039/1073
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/665,248
; PRIOR PELING DATE: 1997-11-13
; PRIOR PELING DATE: 1997-11-11
; PRIOR PELING DATE: 1997-11-11
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; PRIOR PELING DATE: 1997-11-11
; PRIOR PELING DATE: 1999-11-21
; PRIOR PELING DATE: 1999-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR PELING DATE: 1998-10-20
; PRIOR PELING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
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JAPPLICANT: Tomlinson, Ian M
APPLICANT: Winter, Gregory
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 8039/1073B
CURRENT APPLICATION NUMBER: US/09/968,561A
CURRENT APPLICATION NUMBER: GB 972131.1
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
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PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1998-10-20
PRIOR FILING DATE: 2000-02-24
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Sequence 30, Application US/10091300
Publication No. US20030108545A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rockwell, Patricia
APPLICANT: Goldstein, Neil I.
ITILE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular,
ITILE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
FILE REFERENCE: 11245/46211
CURRENT APPLICATION NUMBER: US/10/091,300
CURRENT PILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 85
SOFTWARE: WordPerfect 8.0 for Windows
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Sequence 23, Application US/10091300
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FUBLICATION NO. US20030108545A1
APPLICANT: Rockwell, Patricia
APPLICANT: Goldstein, Neil I.
TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
FILE REFERENCE: 11245/46211
CURRENT APPLICATION NUMBER: US/10/091,300
CURRENT FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 85
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Publication No. US20030108545A1
GENERAL INFORMATION:
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TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular 7 TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist FILE REFERENCE: 11245/46211
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   CAGGCTCCAGGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
   TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACA 240
   cagecrecaseseaasesecrecastesercrearecarrastastastastastastas 174
   CTGTTTCTTCAAATGAACAGCCTGAGAGCTGACACGCTGTCTATTACTGTGTGCGAGC 300
   235 CTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGCTGTGTATTACTGTGCGAGA 294
   175 racracecaeacreaereaaeeecearreacearerecaeeaeaeaeeecaaeaeeea 234
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  TCCTGTGCCAGCCTCTG-----GATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGC
  Gaps
  301 TIGACTACAGGGTCTGACTCCTGGGGCCAGGAGTCCTGGTCACCGTCTC 350
  295 GTCACAGATGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTC 344
  9
  9
   Length 348;
   Length 348;
  67.3%; Score 238.4; DB 15; Length
82.3%; Pred. No. 1.9e-65;
ive 0; Mismatches 56; Indels
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   66.9%; Score 236.8; DB 15;
82.0%; Pred. No. 6e-65;
ive 0; Mismatches 57;
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Best Local Similarity 82.0
Matches 287; Conservative
   Best Local Similarity 82.3
Matches 288; Conservative
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ORGANISM: Human
   TYPE: DNA
CRGANISM: Human
US-10-091-300-27
   US-10-091-300-23
  LENGTH: 348
  LENGTH: 348
  SEQ ID NO 23
   121
  SEQ ID NO 27
  115
   181
   241
   Query Match
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APPLICANT: Foltz, Ian
APPLICANT: Babcock, John
APPLICANT: Babcock, John
APPLICANT: Poltz, Ian
APPLICANT: Babcock, John
APPLICANT: Palathumpat, Raju
APPLICANT: Palathumpat, Raju
APPLICANT: Wing, Chadwick T.
TITLE OF INVENTION: ANTI-CDR4SRB ANTIBODIES FOR USE IN
TITLE OF INVENTION: TREATING AUTOIMMUNE DISEASE AND TRANSPLANT REJECTION
TITLE OF INVENTION: TREATING AUTOIMMUNE DISEASE AND TRANSPLANT REJECTION
FILE REFERENCE: ABGENIX.029A
CURRENT FALING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337,276
PRIOR APPLICATION NUMBER: 60/337,276
PRIOR APPLICATION NUMBER: 60/337,276
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
   393 TACTACGCAGACTCCGTGAAGGGCGGGTTCACCATCTCCAGAGACAATTCCAAGAACAGG 452
  279 TCCTGTGTGCAGCCTCTG-----GATTCACCTTTAGCAGTTTTTCGATGAGCTGGGTCCGC 332
   121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTAGTGATCCCACA 180
  333 caggerecaggaaggggeregagregerererererarragregragregaaceacaea 392
   241 CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGAACACGGCTGTCTATTACTGTGCGAGC 300
   219 daddiecadcigrigdagicigggggggggriggracadccigggggggcccigagacic
  1 GAGGIGCAGCIGGIGGAGICTGGGGGGGCGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
   61 TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC
   301 TIGACTACAGGGICTGACTCCTGGGGCCCAGGGAGTCCTGGTCACCGTCTC 350
  Score 233.6; DB 12; Length 414; Pred. No. 6.4e-64;
   513 ccerrrccerarrradacracredeccadedaacccresrcaccercre
  Indels
  Score 235.2; DB 12;
Pred. No. 3e-64;
  DB 12;
   0; Mismatches
                     PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 96
   Sequence 130, Application US/10309764
Publication No. US20030232009A1
GENERAL INFORMATION:
APPLICATION NUMBER: 09/617,746
   66.0%;
82.3%;
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Best Local Similarity 81.7%;
Matches 286; Conservative
   ; NAME/KEY: CDS
; LOCATION: (162)..(1085)
US-10-291-265-96
   TYPE: DNA ORGANISM: Homo sapiens FEATURE:
  TYPE: DNA ORGANISM: Homo Bapiens
   Query Match
Best Local Similarity
   JS-10-309-764-130
   셤
   Sequence 99, Application US/10291265
Publication No. US20030232054A1
GENERAL INFORMATION:
APPLICANT: Hyeeq, Inc.
APPLICANT: Tang et al
TITLE OF INVENTION: No. US20030232054Alel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-017 (785)
CURRENT FILING DATE: 2000-01-25
FRIOR APPLICATION NUMBER: US/10/291,265
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
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PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
  219 GAGGTGCAGCTGTTGGAGTCTGGGGGGTTGGTACAGCCTGGGGGGTCCCTGAGACTC 278
   TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGGAACGCCAACAACACA 240
   393 TACTACGCAGACTCCGTGAAGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACG 452
   TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 120
  279 TCCTGTGCAGCCTCTG-----GATTCACCTTTAGCAGTTTTTCGATGAGCTGGGTCCGC 332
  CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
   333 CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATCTATTAGTGGTAGTTCGGGTACCACA 392
   241 CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
   CTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAA 512
  Sequence 96, Application US/10291265
Publication No. US20030232054A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tang et al
TITLE OF INVENTION: No. US20030232054A1e1 Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-017 (785)
CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
  Gaps
   301 TTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTC 350
   ccertricceratitricaciacideseccasesaaccerseicacesicie s62
   Length 1710;
   9
   58; Indels
  DB 12;
   Score 235.2; DB Pred. No. 3e-64; 0; Mismatches E
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81.7%;
  Query Match
Best Local Similarity 81.7
Matches 286; Conservative
  , LOCATION: (162)..(1253)
US-10-291-265-99
   TYPE: DNA
ORGANISM: Homo sapiens
   NAME/KEY: CDS
  RESULT 10
US-10-291-265-96
   SEQ ID NO 99
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   235
  122 AGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACAT 181
   293 TGTTTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAA 352
   352
   412
   121
   116 AGGCTCCAGGGAAGGGGCTGGAGTCGGCTATTAGTGGTGGTGGTGGTAGCACAT 175
   233 ACTACGCAGACTCTGTGAAGGGCCGATTCACCATCTCCAGGGCACAAGGAAGTCTCAC 292
  301
   TGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCT 301
   19
  61
   Sequence 66, Application US/10322673

Sequence 66, Application US/10322673

Publication No. US20030180296A1

GENERAL INFORMATION:
APPLICANT: Salced tal.
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF988

CURRENT APPLICATION NUMBER: US/10/322,673

CURRENT APPLICATION NUMBER: 60/341,237

PRIOR PILING DATE: 2002-12-19

PRIOR APPLICATION NUMBER: 60/369,877

PRIOR PILING DATE: 2002-04-05

PRIOR APPLICATION NUMBER: 60/384,828

PRIOR APPLICATION NUMBER: 60/384,828

PRIOR PILING DATE: 2002-06-04

PRIOR FILING DATE: 2002-06-04

PRIOR PILING DATE: 2002-07-18

PRIOR PILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/403,370

PRIOR PILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/403,370

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   353 GGGCGGCTACGGTGACTTTTGACTACTGGGGCCAGGGAACCCTGGTCACGGTCACGTCCT
   62 ccrgrccaccrcrc----GarrcaccrrcaGrGaCtaCtaCarGaGCTGGATCCGCC
  176 acracecagacrecereaagesecesrreacerereceagagacaarrecaagaacaee
  302 TGAC-----TACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCT
   2 AGATGCAGCTGCAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCT
   GGTGCGCAGCCTCCGGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCC
   2 AGGIGCAGCIGGIGGAGICIGGGGGGGCCTIGGCAAAGCCTGGGGGGCTCCTGAGACICT
Gaps
   .
9
   302 TGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTC 350
   DB 13; Length 729;
  Query Match 65.3%; Score 231; DB 13; Length 7 Best Local Similarity 81.1%; Pred. No. 5e-63; Matches 283; Conservative 0; Mismatches 60; Indels
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  ORGANISM: Artificial sequence
   CA 354
  CA 414
   -10-322-673-66
  US-10-322-673-66
   242
   353
  413
  62
   242
   236
  DNA
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  353 GGACTGGATCTACGACGGTCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCT 412
   CCTGTGCAGCCTCTG-----GATTCACCTTCAATGTCTACTACATGAACTGGATCCGCC 172
   | IGTITCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCT 301
  TGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGCCGTGTATTACTGTGCGAGAA 352
  TGACT -----ACAGGGTCTGACTCCTGGGGCCAGGGGTCCTGGTCACCGTCTCCT 352
  59 AGGTGCACCTGGTGCAGTCTGGGGGGGGGCTTGGTCAAGCCTGGAGGTCCTGAGACTCT 118
  121
   119 cerececiaciene----earreacerrearraacracareareacresered
   173 AGGCTCCAGGGAAGGGGCTGGAGTGGGTTTCATACATTAGTCTTAGTGGCAGTACCATAT 232
  AGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACAT 181
  233 actaciciosacticioneras de destros contros de destros de destros de destros de destros de destros de destros de defensas de defensas de defensas de defensas de defensas de defensas de destros de defensas de decensas de defensas de 
  AGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACAT 181
   62 GGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCC 121
   61
   61
  APPLICANT: FOLE, Ian
APPLICANT: Babcook, John
APPLICANT: Babcook, John
APPLICANT: Babcook, John
APPLICANT: Babcook, John
APPLICANT: Yang, Xiao-dong
APPLICANT: Yang, Xiao-dong
APPLICANT: Xing, Chadwick T.
TITLE OF INVENTION: ANTI-DRASRB ANTIBODIES FOR USE IN
TITLE OF INVENTION: TEATING AUTOIMMUNE DISEASE AND TRANSPLANT REJECTION
FILE REFERENCE: ABGENIX.029A
CURRENT APPLICATION NUMBER: US/10/309,764
CURRENT FILING DATE: 2002-12-03
PRIOR FILING DATE: 2001-12-03
  GGTGCGCAGCCTCCGGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCC
  59 Addrecadordeadorordeadeadocriodromadocridaadeacocordaadacoco
  2 AGGTGCAGCTGGTGGAGTCTGGGGGGCCGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTCT
  2 AGGTGCAGCTGGTGGAGTCTGGGGGGGGGCTTGGCAAAGCCTGGGGGGGTCCCTGAGACTCT
  Gaps
             Gaps
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Pred. No. 2.1e-63;
0; Mismatches 50; Indels 15;
             15;
             49; Indels
             0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 126
LENGTH: 414
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   CA 414
  RESULT 12
US-10-309-764-126
  122
  173
   293
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  242
  182
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   353
  TYPE: DNA
             Matches
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   CAGGCTCCAGGGCAGGGCTGGAGTGGGTCTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
   TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACACACA 240
  TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACG 234
  TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 120
   61 recrerecedescricae----earreacerrrascecerarracareacerescrice 114
   CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
   235 CTGTATCTGCAAATGAACAGCCTGAGAGCCGAGAGGACGGCCCTATATTACTGTGCGAGA 294
   1 chégricohocricordohoaccedogadecrirogracodocricododorcocricodadacric 60
   Sequence 1, Application US/09949039; Publication No. US20030166160A1; GENERAL INFORMATION:
APPLICANT: HAWLEY, STEPHEN B.
TITLE OF INVENTION: COMPOUNDS AND MOLECULAR COMPLEXES COMPRISING MULTIPLE; TITLE OF INVENTION: BINDING REGIONS DIRECTED TO TRANSCYTOTIC LIGANDS
   Gaps
   301 TIGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTC 350
  GGGGCATCTGGCCCTGACTACTGGGGCAGAGGGACAATGGTCACCGTCTC 344
   9
296 GAGGATCCACTTTGATATCTGGGGCCGGGGGACAATGGTCACCGTCTC 344
  DB 13; Length 729;
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Pred. No. 7.8e-63;
0; Mismatches 61; Indels
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ORGANISM: Artificial sequence
  Query Match
Best Local Similarity 80.9%;
Matches 283; Conservative
  RESULT 14
US-10-322-673-68
  US-10-322-673-68
  RESULT 15
US-09-949-039-1
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468
  588
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  62 GGTGCGCAGCCTCCGGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCC 121
   528
   589 reinarciecanarenachecreadaccendagaccencececerererarracrereresedene 648
   122 AGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACAT 181
  242 TGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCT 301
   61
   529 ACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAACGCCAAGAACTCAC
   415 ccrerecaecrere----earreaecrreagracrargeaereaece
  302 TGACTACAGGG----TCTGACTCCTGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 354
  2 AGGIGCAGCIGGAGTCTGGGGGCGCTTGGCAAAGCCTTGGGGGGTCCCTGAGACTCT
   649 ATACCCGAGGGTACTTCGATCTCTGGGCCGTGGCACCCTGGTCACCGTCTCCTCA 704
  Gaps
   Description of Artificial Sequence: pSyn5AF DNA sequence
  9.
  DB 13; Length 4026;
  Indels
   ٠..
  26;
   Score 228.4; DB 1:
Pred. No. 5.3e-62;
0; Mismatches 56
   Search completed: December 30, 2003, 03:42:16
Job time : 513.438 secs
FILE REFERENCE: 057220/1301
CURRENT APPLICATION NUMBER: US/09/949,039
CURRENT FILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4026
  TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
   Query Match
Best Local Similarity 81.7%;
Matches 291; Conservative C
   OTHER INFORMATION: OTHER INFORMATION:
  US-09-949-039-1
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